



pD17-cJ-dCH2.H1

10 GACGGATCGG GAGATCTGCT AGGTGACCTG AGGCGCGCGG GCTTCGAATA GCCAGAGTAA CCTTTTTTTT TAATTTTATT TTATTTTATT 90
CTGCCTAGCC CTCTAGACGA TCCACTGGAC TCCGCGCGCG CGAAGCTTAT CCGTCTCAAT GGAAAAAATA ATTAATAATAA AATAATAATAA 80

100 TTTGAGATGG AGTTTGGCGC CGATCTCCCG ATCCCTATG GTCGACTCTC AGTACAATCT GCTCTGATGC CGCATAGTTA AGCCAGTATC 180
AAACTCTACC TCAAAACCGCG GCTAGAGGGC TAGGGGATAC CAGCTGAGAG TCATGTTAGA CGAGACTACG GCGTATCAAT TCGGTCTATAG 170

190 TGCTCCCTGC TTGTGTGTTG GAGGTGCGTG AGTAGTGGC GAGCAAAAT TAAGCTACAA CAAGGCAAGG CTTGACCGAC AATTGCATGA 270
ACGAGGGACG AACACACAAC CTCACAGCGC TCATCAACGG CTCGTTTTAA ATTGATGTT GTTCCGTTCC GAACTGGCTG TTAACGCTACT 260

280 AGAATCTGCT TAGGGTTAGG CGTTTTCGCG TGCTTCGCGA TGTAAGGCGC AGATATACGC GTTGACATTC ATTATTGACT AGTTATTAAAT 360
TCTTAGACGA ATCCCNATCC GCANAAACGCG ACGAAGCGCT ACATGCCCCG TCTATATGCG CAATGTAACT TAATAACTGA TCAATAATAA 350

370 AGTAATCAAT TAGGGGTCA TTAGTTTCAATA GCCCATATAT GCCCATATAT GGAGTTTCGC GTTACATAAC TTACGGTAAA TGGCCCCCT GGCTGACCCG 450
TCATTAGTTA ATGCCCAAGT AATCAAGTAT CCGGTATATA CCGTCAAGCG CCTCAAGTATG CAATGTATTC AATGCCATTT ACCGGCGGA CCGACTGGCG 440

460 CCAACGACCC CCGCCCATTC AGGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCA TGGGTGGACT 540
GGTTGCTGGG GCGGGGTAAC TGCAGTTAAT ACTGCATACA AGGTATATCAT TGCGGTTATC CCTGAAAAGT AACTGCAGTT ACCCACCTGA 530

550 AATTACGGTA AACTGCCCCA TTGGCAGTAC ATCAAGTCTA TCAATATGCCA AGTACGCCCC CTATTGACGT CAATGACGGT AATGCGCCCG 630
TAAATGCCAT TTGACGGGTG AACCGTCAAT TAGTTCACAT AGTATACGGT TCAATGCGGG GCATAACTGCA GTTACTGCCA TTTTACCGGGC 620

640 CCTGGCAATA TGCCCAAGTAC ATGACCTTAT GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAAT CGCTATTACC ATGGTGATGC 720
GGACCGTAAT ACGGTCTATG TACTGGAATA CCTGGAATA ATGAACCGTC ATGATAGATGC ATGATCAAGTATA GCGATATAGG TACCACCTACG 710

730 GGTTTTGGCA GTACATCAAT GGGCGTGGAT ACGCGTTTGA CTTCCAGTCC TTTCCAAAGT TCCACCCCAT TGACGTCAAT GGGAGTTTGT 810
CCAAAAACCGT CATGTAGTTA CCGGCACCTA TCGCCAACT TCGGCTCAG AAGSTTCAG AGGTGGGGTA ACTGCAGTTA CCCTCAACA 800

820 TTTGGCACCA AATCAACCGG GACTTTTCCA AATGTCGTAA CAATCTCGCC CCAATGACGC AAATGGCGG TAGGCGTGA CGGTGGGAGG 900
AAACCGTGGT TTTAGTTGCC CTGAAAGGTT TTACAGCATT GTTGAGGCGG GGTAACTGCG TTTACCGGCC ATCCGCACAT GCCACCCCTCC 890

FIGURE 14A
(SEQ ID NO. 10)

pD17-cJ-dCH2.H1

```

910      920      930      940      950      960      970      980      990
TCTATATAAG CAGAGCTCTC TGGCTTAACTA GAGAACCACAC TGCTTACTGG CTTATATCAAA TTAATACGAC TCACATATAGG GAGACCCCAAG
AGATATATTC GTCTCGAGAG ACCGATGTGAT CTCCTGGGTG ACGAATGACC GNAATAGCTTT AATTATGCTG AGTGATATCC CTTGGGTTC

1000      1010      1020      1030      1040      1050      1060      1070      1080
CTTGGTACCA ATTTAAATTTG ATATCTCTCTT AGGTCTCGAG TCCTCTAGATA ACCGGTCAAT CGATTGGAAT TCCTTGGCGCC GCTTGTCTAGC
GAACCATGGT TAAATTTTAAAC TATAGAGGAA TCCAGAGGTC AGAGATCTAT TGGCCAGTTA GCTAACCTTA AGAACGCCGG CGAACGATCG

1090      1100      1110      1120      1130      1140      1150      1160      1170
CACCATGGAG TTGTGGTTAA GCTTGGTCTT TCCTTGTCTT TGTCTTAAAA GGTGTCAGT GTGAAGTGAA TCTGTGTGGAG TCTGGGGGAG
GTGGTACCTC AACACCAATT CGAACCCAGGA AGGAACAGGA ACAAAATTTT CCACAGGTCA CACTTCACTT AGACCACCTC AGACCCCTC

1180      1190      1200      1210      1220      1230      1240      1250      1260
GCTTAGTGCA GCCTGGAGGG TCCCTGAAAG TCCTCTGTGT AACCTCTGGA TTCACCTTCA GTGACTATTA CATGTATTTG GTTCCGCCAGA
CGAATCACGT CGGACCTCCC AGGACTTTC AGAGGACACA TTGGAGACCT AAGTGAAAGT CACTGATAAT GTACATAAACC CAACGGGTCT

1270      1280      1290      1300      1310      1320      1330      1340      1350
CTCCAGAGAA GAGGCTGGAG TGGGTGCGAT ACAATTAGTCA AGGTGTGTAT ATAACCGACT ATCCAGACAC TGTAAGGGT CGATTTCACCA
GAGGTCTCTT CTCGACCTC ACCGACGTA TGTAATCAGT TCCACCACTA TATTGGCTGA TAGGTCTGTG ACATTTCCCA GCTAAGTGGT

1360      1370      1380      1390      1400      1410      1420      1430      1440
TCTCCAGAGA CAATGCCAAG AACACCTGT ACCTGTCAAT GAGCCGTCTG AAGTCTGAGG ACACAGGCAT GTATTACTGT GCAAGAGGCC
AGAGGTCTCT GTTACGGTTC TTGTGGGACA TGGACGTTTA CTCGGCAGAC TTCAGACTCC TGTTCTGGTA CATAATGACA CGTTCTCCGG

1450      1460      1470      1480      1490      1500      1510      1520      1530
TGGACGACGG GGCTGTGTTT GCTTACTGGG GCCAAGGGAC TCCTGTACAG GTCTCTGTAG CTAGCACCAA GGGCCCATCG GTCTTCCCCC
ACCTGTCTGC CCGGACCAA CGAATGACCC CGGTTCCTCT AGACCAGTGC CAGAGACATC GATCGTGGTT CCCGGGTAGC CAGAAGGGGG

1540      1550      1560      1570      1580      1590      1600      1610      1620
TGGCACCTTC CTCCAAGAGC ACCCTCTGGG GCACAGCGGC CCTGGCTGCG CTGGTCAAGG ACTACTTCCC CGAACCCGTG ACGGTGTCTGT
ACCGTGGGAG GAGGTCTCTG TGGAGACCCC CGTGTGCGCG GGACCCGACG GACCAGTTCC TGATGAAGGG GCTTGGCCAC TGCCACAGCA

1630      1640      1650      1660      1670      1680      1690      1700      1710
GGAACCTCAGG CGCCCTGACC AGCGGCGTGC ACACCTTCCC GGCTGTCTTA CAGTCTCTCAG GACTCTACTC CCTCAGCAGC GTGTCTACCG
CCTTGAGTCC GCGGACTGG TCGCCGACG TGTGGAAGGG CCGACAGGAT GTCAGGAGTC CTGAGATGAG GGAGTCTGCG CACCAGTGGC

1720      1730      1740      1750      1760      1770      1780      1790      1800
TGCCCTCCAG CAGCTTGGGC ACCCAGACCT ACATCTGCAA CGTGAATCAC AAGCCCCAGCA ACACCAAGGT GGACAAGAAA GTTGTGTAGA
ACGGGAGGTC GTCGAACCCG TGGGTCTGGA TGTAGAGGTT GCACTTAGTG TTCGGGTGCT TGTGGTTCCA CCTGTCTTTT CAACCACTCT

```

FIGURE 14B
(SEQ ID NO. 10)

pD17-cJ-dCH2.H1

1810	1820	1830	1840	1850	1860	1870	1880	1890
GGCAGCAC	GGGAGGAG	GTGTCTGT	GAAGCAGC	TCAGCGTCC	TGCTTGACG	CATCCGGCT	ATGCAGCCC	AGTCCAGGGC
CCGTCGTGT	CCCTCCCTCC	CACAGACGAC	CTTCGGTCCG	AGTCGGAGG	ACGGACCTGC	GTAGGCCGA	TACGTGGGG	TCAGGTCCCC
1900	1910	1920	1930	1940	1950	1960	1970	1980
AGCAAGGAG	GCCCCGTCTG	CCCTCTAC	CGGAGGCTC	TGCCCCCCCC	ACTCATCTC	AGGGAGAGG	TCCTTCGGCT	TCTTCCCCCAG
TCGTTCCGTC	CGGGCAGAC	GGAGNAGTG	GCCCTCCGAG	ACGGGCGGG	TGAGTAGAG	TCCCTCTCCC	AGAAAGACCGA	AAAAGGGGTC
1990	2000	2010	2020	2030	2040	2050	2060	2070
GCTCTGGCA	GGCAGAGCT	AGGTGCCCT	AACCCAGGCC	CTGCACACAA	AGGGGAGGT	GCTGGGCTCA	GACCTGCCAA	GAGCCATATC
CGAGACCCGT	CCGTGTCCGA	TCCACGGGA	TTGGGTCCGG	GACGTGTGTT	TCCCCGTCCA	CGACCCGAGT	CTGGACGGTT	CTCGGTATAG
2080	2090	2100	2110	2120	2130	2140	2150	2160
CGGAGGACC	CTGCCCTGA	CCTAAGCCCA	CCCCAAGGC	CAAACTCTCC	ACTCCCTCAG	CTCGGACACC	TTCTCTCTC	CCAGATTCCA
GCCCTCCTGG	GACGGGACT	GGATTCCGGT	GGGGTTTCCG	GTTTGAGAGG	TGAGGGAGTC	GAGCCTGTGG	AAGAGAGGAG	GGTCTAAGGT
2170	2180	2190	2200	2210	2220	2230	2240	2250
GTAACCTCCA	ATCTTCTCTC	TGCAGAGCCC	AAATCTGTG	ACAAACTCA	CACATGCCCA	CCGTGCCCAG	GTAAGCCAGC	CCAGGCTCTG
CATTGAGGGT	TAGAGAGAG	ACGTCTCGGG	TTTAGAACAC	TGTTTGTAGT	GTGTACGGGT	GGCACGGGTC	CATTCCGGTC	GGTCCGGAGC
2260	2270	2280	2290	2300	2310	2320	2330	2340
CCCTCCAGCT	CAAGCGGGA	CAGGTGCCCT	AGAGTAGCCT	GCATCCAGGG	ACACACCACG	TGGGTACCAA	CATGTCCCGA	GCCACATGGA
GGGAGGTGCA	GTTCGCCCT	GTCCACGGGA	TCTCATCGGA	CGTAGGTCCC	TGTGTGTGTC	ACCCATGGTT	GTACAGGCT	CGGTGTACCT
2350	2360	2370	2380	2390	2400	2410	2420	2430
CAGAGCCCG	CTCGGCCAC	CCCTCTGCCCT	GAGAGTGACC	GCTGTACCAA	CCTCTGTCTCC	TACAGGGGCG	CCCCGAGAAC	CACAGGTGTA
GTCTCCGGCC	GAGCCGGGTG	GGAGACGGGA	CTCTCACTGG	CGACATGGTT	GGAGACAGGG	ATGTCCCGTC	GGGGCTCTTG	GTGTCCACAT
2440	2450	2460	2470	2480	2490	2500	2510	2520
CACCTGCCC	CCATCCCGG	ATGAGCTGAC	CAAGAACCCAG	GTCAGCCCTGA	CCGTCCCTGGT	CAAAGGCTTC	TATCCACGG	ACATCCGGCT
GTGGGACGGG	GGTAGGGCCC	TACTCGACTG	GTCTCTGTGC	CAGTCGGACT	GGACGGACCA	GTTTCCGAAG	ATAGGGTCC	TGTAGCGGCA
2530	2540	2550	2560	2570	2580	2590	2600	2610
GGAGTGGAG	AGCAATGGGC	AGCCGGAGAA	CAACTACAG	ACCACGCCCTC	CCGTGCTGGA	CTCCGACGGC	TCCTTCTTCC	TCTACAGCAA
CCTCACCCCTC	TCGTACCCCG	TCGGCCCTCTT	GTTGATGTTT	TGGTCCGGAG	GGCAGGACCT	GAGGCTGCCG	AGGAAGAGAG	AGATGTCTGT
2620	2630	2640	2650	2660	2670	2680	2690	2700
GCTCACCCGTG	GACAAGAGCA	GGTGGCAGCA	GGGGAACGTC	TTCTCATGCT	CCGTGATGCA	TGAGGCTCTG	CACAACCACT	ACACGCAGAA
CGAGTGGCAC	CTGTTCTCGT	CCACCGTCTG	CCCCCTTGCAG	AAGAGTACGA	GGCACTACCT	ACTCCGAGAC	GTGTTGGTGA	TGTGCGTCTT

FIGURE 14C
(SEQ ID NO. 10)

pD17-cJ-dCH2.H1

```

2710 GAGCCTCTCC 2720 CTGCTCTCCG 2730 GTAAATGAGT 2740 GCGACGGCCG 2750 GCAAGCCCCC 2760 GCTCCCCGGG 2770 CTCTCGCGGT 2780 CGCAGGAGGA 2790 TGCTTGGCAC
CTCGGAGAGG GACAGAGGCC CATTTACTCA CGCTGCCGGC CGTTCGGGGG CGAGGGGGCC GAGAGCGCCA GCGTGTCTCT ACGAACCGTG

2800 GTACCCCCCTG 2810 TACATACTTC 2820 CCGGGCGCCC 2830 AGCATGGAAT 2840 TAAAGCACCC 2850 AGCGCTGCCC 2860 TGGGCCCTCTG 2870 CGAGACTGTG 2880 ATGGTTCTTT
CATGGGGGAC ATGTATGAAG GGGCCGCGGG TCGTACCCTT ATTTCTGTGG TCGCGACGGG ACCCGGGGAC GCTCTGACAC TACCAAGAAA

2890 CCACGGGTCA 2900 GGCCGAGTCT 2910 GAGGCTGAG 2920 TGGCATGAGG 2930 GAGGCAGAGC 2940 GGGTCCCACT 2950 GTCCCCACAC 2960 TGGCCCCAGG 2970 TGTGCAAGTG
GGTGCCCACT CCGGCTCAGA CTCCGGACTC ACCGTACTCC CTCCGTCTCG CCCAGGTGA CAGGGGTGT ACCGGGTCCG ACACGTCCAC

2980 TGCCCTGGCC 2990 CCTAGGGTG 3000 GGGCTCAGCC 3010 AGGGCTGCC 3020 CTCGGCAGGG 3030 TGGGGGATTT 3040 GCCAGCGTGG 3050 CCTTCCCTCC 3060 AGCAGCACCT
ACGGACCCCG GGGATCCAC CCGGATCCAC CCGGATCCG TCCCGGACGG GAGCGTCCC ACCCCCTAAA CCGTCCGACC GGGAGGGAGG TCGTCTGTGA

3070 GCCCTGGGCT 3080 GGGCCACGGG 3090 AAGCCCTAGG 3100 AGCCCCTAGG 3110 GACAGACACA 3120 CAGCCCCCTGC 3130 CTCTGTAGGA 3140 GACTGTCTCTG 3150 TTCTGTGAGC
CGGGACCCGA CCGGTGCC CCGGTGCC TCCGGGATCC TCCGGGATCC CTGTCTGTGT GTCTGTGTGT GTGACATCTT CTGACACAGGAC AAGACACTCG

3160 GCCCCCTGTC 3170 TCCCCGACCTC 3180 CATGCCCACT 3190 CCGGGGCGATG 3200 CCTAGTCCAT 3210 GTGCGTAGGG 3220 ACAGGCCCTC 3230 CCTACCCCAT 3240 CTACCCCTAC
CGGGACACAG AGGGCTGGAG GTACGGGTGA GCGGGGTGAC GCGGGGTGAC TACCCCTGTG TTGGCTGAGG CCCCTGTACG TGAGAGCCCG GGACACCTCC

3250 GGCACTAACC 3260 CCTGGCTGCC 3270 CTGCCAGGCC 3280 TCGCACCCGC 3290 ATGGGACAC 3300 AACCGACTCC 3310 GGGGACATGC 3320 ACTCTCGGGC 3330 CCTGTGAGG
CCGTGATTGG GGACCGACGG GACGGGTGG GACGGGTGG AGCGTGGGG TACCCCTGTG TTGGCTGAGG CCCCTGTACG TGAGAGCCCG GGACACCTCC

3340 GACTGTGCA 3350 GATGCCACA 3360 CACACACTCA 3370 GCGGTCTGGG 3380 GTTCAACAAA 3390 CCCCAGCTG 3400 AGGTGGCCG 3410 GCCACACGGC 3420 CACCACACAC
CTGACCAACG CTACGGGTGT GTGTGTGAGT GCGGTCTGGG CCGGTCTGGG CAAAGTTGTT GGGCGGTGAC TCCAACCCCG CCGTGTGCCG GTGCTGTGTTG

3430 ACACGTGCAC 3440 GCCTCACA 3450 CCGAGCCTCA 3460 CCGGGCGGAA 3470 CTGCACAGCA 3480 CCCAGACCCAG 3490 AGCAAGTCC 3500 TCGCACACGT 3510 GNAACCTCTT
TGTGCACGT CCGAGTGTGT GCCTCGGAGT GGGCCCGCTT GACGTGTCGT GCGTCTGGTC TCGTCCAGG AGCGTGTGCA CTTGTGAGGA

3520 CGGACACAGG 3530 CCCCCACAG 3540 CCCCACGGG 3550 CACCTCAGG 3560 CCCACGAGCC 3570 TCTCGGCAGC 3580 TTCTCCACAT 3590 GCTGACCTGC 3600 TCAGACAAAC
GCCTGTGTCC GGGGTGCTC GGGGTGCTC GGGGTGCTC GGGGTGCTC GGGGTGCTC GGGGTGCTC GGGGTGCTC GGGGTGCTC GGGGTGCTC

```

FIGURE 14D
(SEQ ID NO. 10)

pD17-cJ-dCH2.H1

3610 CCAGCCCTCC TCTCACAAGG 3620 GTGCCCTGCG 3630 AGCCGCCACA 3640 CACACACAGG 3650 GGATCACACA 3660 CCACGTCACG 3670 TCCCTGGCCC 3680 TGGCCCACTT 3690
 GGTGGGAGG AGAGTGTTC CACGGGACG TCGGCGGTGT TCGGCGGTGT GTGTGTGTC CCTAGTCTGT GTGTCACGTC AGGACCGGG ACCCGGTGAA
 3700 CCCAGTGCCG CCCTTCCCTG 3710 CAGGACGGAT 3720 CAGCCCTGAC 3730 TGTCCTTCT AGTTGCCAGC 3740 CATCTGTGT TTGCCCTTCC 3750 AACGGGAGG 3760 CCCGTGCTTT
 GGGTCACGGC GGAAGGGAC GTCTTGCTA GTCCGTGCTA GTCCGTGCTA GTCCGTGCTA TCAACGGTGT GTAGACAACA AACGGGAGG GGGCAGGAA
 3790 CCTTGACCTT GGAAGGTGCC 3800 ACTCCACTG 3810 TCCCTTCCCTA 3820 ATAAATGAG 3830 GAAATTCGAT 3840 CGCATTTGCT 3850 GAGTAGGTGT 3860 CATCTATTTC
 GGAACGTGGG CCTTCCACGG TGAAGGTGAC AGGAAAGGAT TATTTTACTC TATTTTACTC CCGTAACAGA CTCATCCACA GTAAGATAAG
 3880 TGGGGGGTGG GGTGGGGCAG 3890 GACAGCAAGG 3900 GGGAGGATG 3910 GGAAGACAAT 3920 AGCAGGATG 3930 CTGGGATGTC 3940 GGTGGGCTCT 3950 ATGGCTTCTG
 ACCCCGCCAC CCACCCGTC CTGTGCTTCC CCTTCTTAAC CCTTCTGTTA TCGTCCGTAC GACCCCTACG CCACCCGAGA TACCGAAGAC
 3970 AGCGGGAAG AACCACTGG 3980 GGCCTTAGGG 3990 GGTATCCCA 4000 CGCGCCCTGT 4010 AGCGGCGCAT 4020 TAAGCGCGG 4030 GGGTGTGGTG 4040 GTTACGCGCA
 TCCGCTTTC TTGGTCGACC CCGAGATCCC CCATAGGGGT GCGCGGACA GCGCGGCTA ATTCGCGCG CCCACACACG CAATGCGCGT
 4060 GCGTGACCGC TACACTTCCC 4070 AGCGCCCTAG 4080 CGCCCGCTCC 4090 TTTTCGGTTTC 4100 TTTCCCTTCTT 4110 TTCTCGCCAC 4120 GTTCGCGGG 4130 CCTTCTCAAA
 CGCACTGGCG ATGTGAACGG TCGCGGGATC TCGCGGGAGG AAAGCGAAG AAGAGCGGTG CAAGCGGCGG CAAGCGGCGG GGAGAGTTT
 4150 AAGGGAATAA AAGCATGCAT 4160 CTCATATAGT 4170 CAGCAACCAT 4180 AGTCCCGCCC 4190 CTAACCTCCG 4200 CCATCCCGCC 4210 CCACTCCCGC 4220 CCCAGTTCCG
 TTCCCTTTT TTCTGTAGTA GAGTTAATCA GTCTGTGTA TCAGGCGCGG GATTGAGCG GTTAGGCGG GATTGAGCG GGTCAAGGC
 4240 CCCATTCTCC GCGCCATGGC 4250 TGACTAATTT 4260 TTTTATTATTA 4270 TGCAGAGGCC 4280 GAGGCGCGCT 4290 CGGCCCTCTGA 4300 GCTATTCCAG 4310 AAGTAGTGAG
 GGGTAAGAGG CGGGGTACCG ACTGATTAA AAAATAAAT AAAATAAAT TGTCTCCCG CTCCCGCGGA CCGCGAGACT CGATAAGGTC TTCATCACTC
 4330 GAGGCTTTT TGAAGGCCTA 4340 GGCCTTTGCA 4350 AAAAGCTGG 4360 ACAGCTCAGG 4370 GCTGCAATTT 4380 CGCGCAAAAC 4390 TTGACGGCAA 4400 TCCTAGCGTG
 CTCGGAATAA ACCTCCGGAT 4410 CCGAATAACGT 4420 TTTTGAACCT 4430 TGTCTGATCC 4440 CGACGTAATA GCGCGGTG AACTGCGGT AGGATCGCAC
 4420 AAGGCTGGTA 4430 GATTTTATC 4440 CCGCTGCCA 4450 TCATGGTTCC 4460 ACCATTGAAC 4470 TGCATCGTCG 4480 CCGTGTCCCA 4490 AAATATGGG 4500 ATTGGCAAGA
 TTCCGACCAT CCTAAAAATAG GGGGACGGT AGTACCAAGC TGGTAATTTG ACGTAGCAGC GGCACAGGGT TTTATACCCC TAACCGTTCT

 FIGURE 14E
 (SEQ ID NO. 10)

pD17-cJ-dCH2.H1

4510	ACGGAGACCT	4520	ACCTTGGCCT	4530	CCGCTCAGGA	4540	ACGAGTTCAA	4550	GTACTTCCAA	4560	AGAAATGACCA	4570	CAACCTCTTC	4580	AGTGAAGGT	4590	AAACAGAAATC
	TGCCCTCTGA		TGGGACCGGA		GGCGAGTCCT		TGCTCAAGTT		CAAGAAGGTT		TCCTACTGGT		GTTCGAGAAG		TCACCTTCCA		TTTGTCTTAG
4600	TGGTGATTAT	4610	GGGTAGGAAA	4620	ACCTGGTTCT	4630	CCATTCCTGA	4640	GAAGAATCGA	4650	CCCTTAAAGG	4660	ACAGAAATTA	4670	TATAGTTCTC	4680	AGTAGAGAAC
	ACCACTAATA		CCCATCCTTT		TGGACCAAGA		GGTAAGGACT		CTTCTTAGCT		GGAATTTCC		TGCTCTTAAT		ATATCAAGAG		TCATCTCTTG
4690	TCAAAGAACC	4700	ACCACGAGGA	4710	GCTCATTTTC	4720	TTGCCAAAG	4730	TTTGGATGNT	4740	GCCTTAAAGAC	4750	TTATTTGAACA	4760	ACCGAAATG	4770	GCAAGTAAAG
	AGTTTCTTGG		TGGTGCTCCT		CGAGTAAAG		AACGGTTTTC		AACTTACTA		CGGAATTTCTG		AAATACTTGT		TGGCCTTAAC		CGTTCAATTC
4780	TAGACATGGT	4790	TTGGATAGTC	4800	GGAGGCAGTT	4810	CTGTTTACCA	4820	GGAAGCCATG	4830	AATCAACCAG	4840	GCCACCTTAG	4850	ACTCTTTGTG	4860	ACAAGGATCA
	ATCTGTACCA		AACCTATCAG		CCTCCGTCAA		GACAAATGGT		CCTTCGGTAC		TTAGTTGGTC		CGGTGGAATC		TGAGAAACAC		TGTTCTCTAGT
4870	TGCAGGAATT	4880	TGAAAGTGAC	4890	ACGTTTTC	4900	CAGAAATGA	4910	TTTGGGAAA	4920	TATAAACTTC	4930	TCCCAAGATA	4940	CCCAGGCGTC	4950	CTCTCTGAGG
	ACGTCTCTAA		ACTTTCAC		TGCAAAAGG		GTCTTTAACT		AAACCCCTTT		ATATTTGAAG		AGGGTCTTAT		GGGTCCGCAG		GAGAGACTCC
4960	TCCAGGAGGA	4970	AAAAGGCATC	4980	AAGTATAAGT	4990	TTGAAGTCTA	5000	CGAGAAGAAA	5010	GACTAAACAGG	5020	AAGATGCTTT	5030	CAAGTTCTCT	5040	GCTCCCTCC
	AGGTCTCTCT		TTTTCCGTAG		TTTCATATCA		AACCTCAGAT		GCCTTCTCTT		CTGATTTGTC		TTCTACGAAA		GTTCAAGAGA		CGAGGGGAGG
5050	TAAAGCTATG	5060	CATTTTATA	5070	AGACCATGGG	5080	ACTTTTGCTG	5090	GCTTTAGATC	5100	TCCTTTGTAA	5110	GGAACCTTAC	5120	TTCTGTGGTG	5130	TGACATNAAT
	ATTTGATAC		GTAATAATAT		TCTGGTACCC		TGAATAACGAC		CGAAATCTAG		AGAAACACTT		CCTTGGAAATG		AAGACACCAC		ACTGTATTAA
5140	GGACAAACTA	5150	CCTACAGAGA	5160	TTTAAAGCTC	5170	TAAGGTAAAT	5180	ATAAATTTT	5190	TAAGTGATA	5200	ATGTGTTAAA	5210	CTACTGATTC	5220	TAATGTGTTG
	CCTGTTTGAT		GGATGTCCT		AAATTTTCGAG		ATTCCATTTA		TATTTTAAAA		ATTCACATAT		TACACAATTT		GATGACTAAG		ATTACAAAAC
5230	TGTAATTTTAG	5240	ATTCCAACCT	5250	ATGGAACCTGA	5260	TGAATGGGAG	5270	CAGTGGTGA	5280	ATGCTTTTAA	5290	TGAGGAAAAC	5300	CTGTTTGTCT	5310	CAGAAGAAAT
	ACATAAAATC		TAAGGTTGGA		TACCTTGACT		ACTTACCCTC		GTCACCACCT		TACGGAATTT		ACTCTCTTTG		GACAAAACGA		GTCTTCTTTA
5320	GCCATCTAGT	5330	GATGATGAGG	5340	CTACTGCTGA	5350	CTCTCAACAT	5360	TCCTACTCCTC	5370	CAAAAAGAA	5380	GAGAAAGGTA	5390	GAAGACCCCA	5400	AGGACTTTCC
	CGGTAGATCA		CTACTACTCC		GATGACGACT		GAGAGTTGTA		AGATGAGGAG		GTTTTTCTT		CTCTTTCCAT		CTTCTGGGGT		TCCTGAAAGG

FIGURE 14F
(SEQ ID NO. 10)

pD17-cJ-dCH2.H1

5410 TTCAGAAATG CTAAGCTTTT TGAGTCATGC 5430 TGCTGTAGT 5440 AATGAACTC 5450 TTGCTGCTT 5460 ACCCAAAGG 5480 ACCAAAGG 5490 AAAAAAGTGC
AAGTCTTAAC GATTCAAAA ACTCAGTACG 5420 TGCTGTAGT 5430 TGCTGTAGT 5440 AATGAACTC 5450 TTGCTGCTT 5460 ACCCAAAGG 5480 ACCAAAGG 5490 AAAAAAGTGC
5500 ACTGCTATAC AAGAAATTA TGGAAAAATA 5520 TTCTGTAACTC 5530 TTTATTAAGTA 5540 GGCAATACAG 5550 TTATTAATCAT 5560 AACATACTGT 5570 TTTTCTTAC
TGACGATATG TTCCTTTAAT ACCCTTTTAT 5510 TTTATTAAGTA 5520 TTCTGTAACTC 5530 TTTATTAAGTA 5540 GGCAATACAG 5550 TTATTAATCAT 5560 AACATACTGT 5570 TTTTCTTAC
5590 TCCACACAGG CATAGAGTGT CTGCTATTA 5600 TAACTATGCT 5610 TAACTATGCT 5620 TAACTATGCT 5630 TAACTATGCT 5640 TAACTATGCT 5650 TAACTATGCT 5660 TAACTATGCT 5670 TAACTATGCT
AGGTGTGCTC GTATCTCACA GACGATAAT 5680 TAACTATGCT 5690 TAACTATGCT 5700 TAACTATGCT 5710 TAACTATGCT 5720 TAACTATGCT 5730 TAACTATGCT 5740 TAACTATGCT 5750 TAACTATGCT 5760 TAACTATGCT
ATATTGTATG TATAGTGCTT 5770 TATAGTGCTT 5780 TATAGTGCTT 5790 TATAGTGCTT 5800 TATAGTGCTT 5810 TATAGTGCTT 5820 TATAGTGCTT 5830 TATAGTGCTT 5840 TATAGTGCTT 5850 TATAGTGCTT
TATAAACTAC ATATCAGGA ACTGATCTCT 5760 TATAGTGCTT 5770 TATAGTGCTT 5780 TATAGTGCTT 5790 TATAGTGCTT 5800 TATAGTGCTT 5810 TATAGTGCTT 5820 TATAGTGCTT 5830 TATAGTGCTT 5840 TATAGTGCTT 5850 TATAGTGCTT
5770 TCCCTCTGAA CCTGAAACAT 5780 TCCCTCTGAA 5790 TCCCTCTGAA 5800 TCCCTCTGAA 5810 TCCCTCTGAA 5820 TCCCTCTGAA 5830 TCCCTCTGAA 5840 TCCCTCTGAA 5850 TCCCTCTGAA
AGGGGACCTT GGACTTTGTA 5760 TCCCTCTGAA 5770 TCCCTCTGAA 5780 TCCCTCTGAA 5790 TCCCTCTGAA 5800 TCCCTCTGAA 5810 TCCCTCTGAA 5820 TCCCTCTGAA 5830 TCCCTCTGAA 5840 TCCCTCTGAA 5850 TCCCTCTGAA
5860 TCACAAATTT CACAAATTA 5870 TCACAAATTT 5880 TCACAAATTT 5890 TCACAAATTT 5900 TCACAAATTT 5910 TCACAAATTT 5920 TCACAAATTT 5930 TCACAAATTT 5940 TCACAAATTT 5950 TCACAAATTT
AGTGTTTAAA GTGTTTATTT 5860 TCACAAATTT 5870 TCACAAATTT 5880 TCACAAATTT 5890 TCACAAATTT 5900 TCACAAATTT 5910 TCACAAATTT 5920 TCACAAATTT 5930 TCACAAATTT 5940 TCACAAATTT 5950 TCACAAATTT
5950 GCTGGATGAT CTTCCAGCG 5960 GCTGGATGAT 5970 GCTGGATGAT 5980 GCTGGATGAT 5990 GCTGGATGAT 6000 GCTGGATGAT 6010 GCTGGATGAT 6020 GCTGGATGAT 6030 GCTGGATGAT 6040 GCTGGATGAT 6050 GCTGGATGAT
CGACCTACTA GGAGGTGCG 5960 GCTGGATGAT 5970 GCTGGATGAT 5980 GCTGGATGAT 5990 GCTGGATGAT 6000 GCTGGATGAT 6010 GCTGGATGAT 6020 GCTGGATGAT 6030 GCTGGATGAT 6040 GCTGGATGAT 6050 GCTGGATGAT
6040 GCAATAGCAT CACAAATTT 6050 GCAATAGCAT 6060 GCAATAGCAT 6070 GCAATAGCAT 6080 GCAATAGCAT 6090 GCAATAGCAT 6100 GCAATAGCAT 6110 GCAATAGCAT 6120 GCAATAGCAT 6130 GCAATAGCAT 6140 GCAATAGCAT 6150 GCAATAGCAT
CGTTATCGTA GTGTTTAAAG 6040 GCAATAGCAT 6050 GCAATAGCAT 6060 GCAATAGCAT 6070 GCAATAGCAT 6080 GCAATAGCAT 6090 GCAATAGCAT 6100 GCAATAGCAT 6110 GCAATAGCAT 6120 GCAATAGCAT 6130 GCAATAGCAT 6140 GCAATAGCAT 6150 GCAATAGCAT
6130 TCTGTATACC GTCGACCTCT 6140 TCTGTATACC 6150 TCTGTATACC 6160 TCTGTATACC 6170 TCTGTATACC 6180 TCTGTATACC 6190 TCTGTATACC 6200 TCTGTATACC 6210 TCTGTATACC 6220 TCTGTATACC 6230 TCTGTATACC 6240 TCTGTATACC 6250 TCTGTATACC 6260 TCTGTATACC 6270 TCTGTATACC 6280 TCTGTATACC 6290 TCTGTATACC 6300 TCTGTATACC
AGACATATGG CAGCTGGAGA 6130 TCTGTATACC 6140 TCTGTATACC 6150 TCTGTATACC 6160 TCTGTATACC 6170 TCTGTATACC 6180 TCTGTATACC 6190 TCTGTATACC 6200 TCTGTATACC 6210 TCTGTATACC 6220 TCTGTATACC 6230 TCTGTATACC 6240 TCTGTATACC 6250 TCTGTATACC 6260 TCTGTATACC 6270 TCTGTATACC 6280 TCTGTATACC 6290 TCTGTATACC 6300 TCTGTATACC
ACACATACG AGCGGGAAGC 6220 TCTGTATACC 6230 TCTGTATACC 6240 TCTGTATACC 6250 TCTGTATACC 6260 TCTGTATACC 6270 TCTGTATACC 6280 TCTGTATACC 6290 TCTGTATACC 6300 TCTGTATACC
TGTTGTATGC TCGGCTTTCG 6220 TCTGTATACC 6230 TCTGTATACC 6240 TCTGTATACC 6250 TCTGTATACC 6260 TCTGTATACC 6270 TCTGTATACC 6280 TCTGTATACC 6290 TCTGTATACC 6300 TCTGTATACC

FIGURE 14G
(SEQ ID NO. 10)

pD17-cJ-dCH2.H1

```

6310      6320      6330      6340      6350      6360      6370      6380      6390
CTTCCAGTC  GGGAAACCTG  TCGTGCCACG  TGCATTAATG  AATCGGCCAA  CGCGCGGGA  GAGGCGGTTT  GCGTATTGGG  CGCTCTTCCG
GAAAGGTCAG  CCTTTGGAC  AGCAGGGTCG  ACCTAATTAC  TTAGCGGGTT  GCGCGCCCT  CTCGCCCAA  CGCATRACCC  GCGAGAAGGC

6400      6410      6420      6430      6440      6450      6460      6470      6480
CTTCCCTCGT  CACTGACTCG  CTGCGCTCGG  TCGTTCCGGT  GCGGCGAGCG  GTATACGCTC  ACTCAAAGGC  GGTAAATACG  TTATCCACAG
GAAGGAGCGA  GTGACTGAGC  GACCGGAGCC  AGCAAGCCGA  CCGCGCTCGC  CATAGTCGAG  TGAGTTTCCG  CCATTATGCC  AATAGGTGTC

6490      6500      6510      6520      6530      6540      6550      6560      6570
AATCAGGGGA  TAACGCGCGA  AAGAACATGT  GAGCAAAAGG  CCAGCAAAAG  OCCAGGAACC  GTAAAAGGC  GCGGTGCTG  GCGTTTTC
TTAGTCCCTT  ATTCCGTCTT  TTCTTGTA  CTCGTTTCC  GGTGTTTTC  CCGTCTTGG  CATTTTCCG  GCGCAACGAC  CGCAAAAAGG

6580      6590      6600      6610      6620      6630      6640      6650      6660
ATAGGCTCCG  CCCCCTGAC  GAGCATACCA  AAAATCGACG  CTCAAAGTCAG  AGGTGGCGAA  ACCCGACAGG  ACTATAAAGA  TACCAGGCGT
TATCCGAGGC  GGGGGACTG  CTCGTAGTGT  TTTTAGCTGC  GAGTTCAATC  TCCACCCTT  TGGGCTGTCC  TGATATTTCT  ATGCTCCGCA

6670      6680      6690      6700      6710      6720      6730      6740      6750
TTCCCCCTGG  AAGCTCCCTC  GTGCGCTCTC  GTGTTCCGAC  CCTGCCGCTT  ACCGGATACC  TGTCCCGCTT  TCCTCCCTTCG  GGAAGCGTGG
AAGGGGGACC  TTCGAGGGAG  CACGCGAGAG  GACRAGGCTG  GGACGGCGAA  TGGCCTATGG  ACAGGCGGAA  AGAGGGGAAGC  CCTTCGGCAC

6760      6770      6780      6790      6800      6810      6820      6830      6840
CGCTTTCTCA  ATGCTCACGC  TGTAGGTATC  TCAGTTTCGT  GTAGGTCTGT  CGCTCCACGC  TGGGCTGTGT  GCACGAACCC  CCCGTTACGC
CGGAAGAGT  TACGAGTGG  ACATCCATAG  AGTCAAGCCA  CATCCAGCAA  GCGAGGTTGC  ACCCGACACA  CGTCTGTGG  GGGCAAGTGG

6850      6860      6870      6880      6890      6900      6910      6920      6930
CCGACCGCTG  CGCCTTATCC  GGTAACATATC  GTCTTGATGC  CAACCCGGTA  AGACACGACT  TATCCGCCACT  TATCCGCCACT  ACTGTAACA
GGCTGGCGAC  GCGGAATAGG  CCATTGATAG  CAGAACTCAG  GATGCTCAA  GATGCTCAA  ACCGGATTGA  TGGCGATGTG  ATCTTCTCTGT  CATAAACCAT

6940      6950      6960      6970      6980      6990      7000      7010      7020
GGATTAGCAG  AGCGAGGTAT  GTAGGCGGTG  CTACAGAGTT  CTTGAAGTGG  TGGCCTNACT  ACGGCTACAC  TAGAAGGACA  GTATTGTTGA
CCTAATCGTC  TCGCTCCATA  CATCCGCCAC  GATGCTCAA  GATGCTCAA  ACCGGATTGA  TGGCGATGTG  ATCTTCTCTGT  CATAAACCAT

7030      7040      7050      7060      7070      7080      7090      7100      7110
TCTGCGCTCT  GCTGAAGCCA  GTTACCTTCG  GAAAAGAGT  TGGTAGCTCT  TGAATCCGCA  AACAAACCA  CGCTGGTAGC  GGTGGTTTTT
AGACGCGAGA  CGACTTCGGT  CAATGGAGC  CTTTTCCTCA  ACCATCGAGA  ACTAGGCCCT  TTTGTTGGTG  GCGACCATCG  CCACCAAAA

7120      7130      7140      7150      7160      7170      7180      7190      7200
TTGTTTGCAA  GCGACGAGTT  ACCGCGAGAA  AAAAGGATC  TCAAGAAGAT  CCTTGTATCT  TTTCTACGGG  GTCTGACGCT  CAGTGGAAACG
AACAAACGTT  CCGCTGCTAA  TCGCGCTCTT  TTTTCTCTAG  AGTTCTCTA  GGAACACTAGA  AAGATGCC  CAGACTGCGA  GTCACCTTGC

```

FIGURE 14H
(SEQ ID NO. 10)

pD17-cJ-dCH2.H1

7210	AAAACTCACG	7220	TTAAGGATT	7230	TTGGTCATGA	7240	GATTATCAA	7250	AAGATCTTC	7260	ACCTAGATCC	7270	TTTTAAATTA	7280	AAAATGAAGT	7290	TTTAAATCAA
	TTTGTAGTGC		AATTCCTTAA		AACCAGTACT		CTAATAGATT		TTCTTAGAAG		TGGATCTAGG		AAATTTAAT		TTTTACTTCA		AAATTTAGTT
7300	TCTAAAGTAT	7310	ATATGAGTAA	7320	ACTTGGTCTG	7330	ACAGTTACCA	7340	ATGCTTAATC	7350	AGTGAGGCAC	7360	CTATCTCAGC	7370	GATCTGTCTA	7380	TTTCTGTTTCA
	AGATTTTCATA		TATACTCAT		TGAACCCAGAC		TGTCAAATGGT		TACGAATTAG		TCACCTCCGIG		GATAGAGTGC		CTAGACAGAT		AAAGCAAGTA
7390	CCATAGTTGC	7400	CTGACTCCCC	7410	GTCTGTGTAGA	7420	TAACTACGAT	7430	ACGGGAGGGC	7440	TTACCANTCIG	7450	GCCCCAGTGC	7460	TGCAATGATA	7470	CCGCGAGACC
	GGTATCAACG		GACTGAGGGG		CAGCACATCT		ATTGATGCTA		TGCCCTCCCG		ATUGGTAGAC		CGGGTCCAGC		ACGTTACTAT		GGCGCTCTGG
7480	CACGTCACCC	7490	GGCTCCAGAT	7500	TTATCAACAA	7510	TAAACCCAGCC	7520	AGCCGGNAAG	7530	GCCGAGCGCA	7540	GAAGTGGTCC	7550	TGCAACTTTA	7560	TCCGGCTCCA
	GTCCGAGTGG		CCGAGGTCTA		AATAGTCTGT		ATTGTGTCGG		TCGGCCCTTCC		CGGCTCCGCT		CITTCACCAGG		ACGTTGANAAT		AGGCGGAGGT
7570	TCCAGTCTAT	7580	TAATTCGTTG	7590	CGGGAAGCTA	7600	GAGTAAGTAG	7610	TTCCGCCAGTT	7620	AATAGTTTGC	7630	GCAAGTGTGT	7640	TGCCATTTGCT	7650	ACAGGCATCG
	AGGTCAGATA		ATTAAACAACG		GCCCTTCCGAT		CTCATTCATC		AAAGCGGTCAA		TTATCAAAACG		CGTTGCAACA		ACGGTAACGA		TGTCCGTAGC
7660	TGGTGTACAG	7670	CTCGTCGTTT	7680	GGTATGGCTT	7690	CATTCAAGTC	7700	CGATCAAGGC	7710	GAGTTACATG	7720	ATCCCCCATG	7730	ATCCCCGTAC	7740	TTGTGCAAAA
	ACCACAGTGC		GAGCAGCAAA		CCATACCGAA		GTAAGTCCAG		GCCAAAGGGTT		GCTAGTTCCG		CTCAATGTAC		TAGGGGTAC		AACAGCTTTT
7750	AAGCGGTTAG	7760	CTCCTTCGGT	7770	CCTCCGATCG	7780	TTGTCAGAAG	7790	TTAGTTGGCC	7800	GCAGTGTATT	7810	CACATCATGGT	7820	TATGGCAGCA	7830	CTGCATAAAT
	TTCCGCCAATC		GAGGAAGCCA		GGAGGCTAGC		AACAGTCTTC		ATTCAACCCGG		CGTCACAATA		GTAGATACCA		ATACCGTCTG		GACGTATTAA
7840	CTCTTACTGT	7850	CATGCCATCC	7860	GTAAGATGCT	7870	TTTCTGTGAC	7880	TGGTGAAGTAC	7890	TCAACCAAGT	7900	CATTCTGAGA	7910	ATAGTGTATG	7920	CGGCGACCGA
	GAGAATGACA		GTACGGTAGG		CATTCTACGA		AAAGACACTG		ACCACTCATG		AGTTGGTTCA		GTAAGACTCT		TATCACATAC		GCCGCTGGCT
7930	GTTGCTCTTG	7940	CCCGGCGTCA	7950	ATACGGGATA	7960	ATACCGGCC	7970	ACATAGCAGA	7980	ACTTTAAAG	7990	TGCTCATCAT	8000	TGGAAACGT	8010	TCITCGGGGC
	CAACGAGAAC		GGGCGGCAGT		TATGCCCTAT		TATGGCGCGG		TGTATCGTCT		TGAAATTTTC		ACGAGTAGTA		ACCTTTTGCA		AGAACCCCGC
8020	GAAACCTCTC	8030	AAGGATCTTA	8040	CCGCTGTGTA	8050	GATCCAGTTC	8060	GATGTAACCC	8070	ACTCGTGCAC	8080	CCAACATGATC	8090	TTCAGCATCT	8100	TTTACTTTCA
	CTTTTGAGAG		TTCTCTAGANT		GGCGACAAC		CTAGGTCAAAG		CTACATTGGG		TGAGCACGTG		GGTTGACTAG		AAGTCGTAGA		AAATGNAAGT

FIGURE 14I
(SEQ ID NO. 10)

pD17-cJ-dCH2.H1

8110	8120	8130	8140	8150	8160	8170	8180	8190
CCAGCGTTTC	TGGGTGAGCA	AAAACAGGAA	GGCAAAATGC	CGCAAAAAG	GGAATAAGG	CGACACGGAA	ATGTTGAATA	CTCATACTCT
GGTCGCAAAG	ACCCACTCGT	TTTTGTCCCT	CCGTTTACG	GGGTTTTTC	CCTTATTC	GCTGTGCCCT	TACAACTTAT	GAGTATGAGA
8200	8210	8220	8230	8240	8250	8260	8270	8280
TCCTTTTTCA	ATATTATTGA	AGCATTTATC	AGGGTTATTG	TCTCATGAGC	GGATACATAT	TTGAANTGTAT	TTAGAAAAT	AAACAATAG
AGGAAAAAGT	TATAANTAAT	TCGTAAATAG	TCCCAATAAC	AGAGTACTCG	CCTATGTATA	AACTTACATA	AATCTTTTAA	TTTGTTTATC
8290	8300	8310	8320	8330				
GGGTCCGCG	CACATTTCCC	CGAAAAGTGC	CACCTGACGT	C				
CCCAAGGCGC	GTGTAAGGG	GCTTTTCACG	GTGGACTGCA	G				

FIGURE 14J
SEQ ID NO. 10)

FIGURE 18A (SEQ ID NO. 22)

```
1  GGTACCAATT TAAATTGATA TCTCCTTAGG TCTCGAGTCT CTAGATAACC
51  GGTCAATCGA TTGGAATTCT TGCGGCCGCT TGCTAGCCAC CATGGAGTTG
101 TGGTTAAGCT TGGTCTTCCT TGTCTTGTT TTAAGAGTG TCCAGTGTGA
151 AGTGCAACTG GTGGAGTCTG GGGGAGGCTT AGTGCAGCCT GGAGGGTCCC
201 TGCGACTTTC CTGTGCTGCA TCTGGATTCC CGTTCAGTGA CTATTACATG
251 TATTGGGTTC GCCAGGCTCC AGGCAAGGGA CTGGAGTGGG TCTCATACAT
301 TAGTCAAGAT GGTGATATAA CCGACTATGC AGACTCCGTA AAGGGTCTGAT
351 TCACCATCTC CAGAGACAAT GCAAAGAACA GCCTGTACCT GCAAATGAAC
401 AGCCTGAGGG ACGAGGACAC AGCCGTGTAT TACTGTGCAA GAGGCCTGGC
451 GGACGGGGCC TGGTTTGCTT ACTGGGGCCA AGGGACTCTG GTCACGGTCT
501 CTTCCGCTAG CACCAAGGGC CCATCGGTCT TCCCCCTGGC ACCCTCCTCC
551 AAGAGCACCT CTGGGGGCAC AGCGGCCCTG GGCTGCCTGG TCAAGGACTA
601 CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC CTGACCAGCG
651 GCGTGACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT CTACTCCCTC
701 AGCAGCGTGG TCACCGTGCC CTCCAGCAGC TTGGGCACCC AGACCTACAT
751 CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTGGAC AAGAAAGTTG
801 GTGAGAGGCC AGCACAGGGA GGGAGGGTGT CTGCTGGAAG CCAGGCTCAG
851 CGCTCCTGCC TGGACGCATC CCGGCTATGC AGCCCCAGTC CAGGGCAGCA
901 AGGCAGGCCC CGTCTGCCTC TTCACCCGGA GGCCTCTGCC CGCCCCACTC
951 ATGCTCAGGG AGAGGGTCTT CTGGCTTTTT CCCCAGGCTC TGGGCAGGCA
1001 CAGGCTAGGT GCCCCTAACC CAGGCCCTGC ACACAAAGGG GCAGGTGCTG
1051 GGCTCAGACC TGCCAAGAGC CATATCCGGG AGGACCCTGC CCCTGACCTA
1101 AGCCCACCCC AAAGGCCAAA CTCTCCACTC CCTCAGCTCG GACACCTTCT
1151 CTCCTCCAG ATTCCAGTAA CTCCCAATCT TCTCTCTGCA GAGCCCAAAT
1201 CTTGTGACAA AACTCACACA TGCCACCGT GCCCAGGTAA GCCAGCCCAG
1251 GCCTCGCCCT CCAGCTCAAG GCGGGACAGG TGCCCTAGAG TAGCCTGCAT
1301 CCAGGGACAG GCCCCAGCCG GGTGCTGACA CGTCCACCTC CATCTCTTCC
```

1351 TCAGCACCTG AACTC²³⁵~~CTGG~~ ²³⁷~~GGAC~~CGTCA GTCTTCCTCT TCCCCCAAA
 1401 ACCCAAGGAC ACCCTCATGA TCTCCCGGAC CCCTGAGGTC ACATGCGTGG
 1451 TGGTGGACGT GAGCCACGAA GACCCTGAGG TCAAGTTCAA CTGGTACGTG
 1501 GACGGCGTGG AGGTGCATAA TGCCAAGACA AAGCCGCGGG AGGAGCAGTA
 1551 CAACAGCACG TACCGTGTGG TCAGCGTCCT CACCGTCCTG CACCAGGACT
 1601 GGCTGAATGG CAAG³¹⁸~~GAGTAC~~ ³²⁰~~AAGTGC~~³²²~~AAGG~~ TCTCCAACAA AGCCCTCCCA
 1651 ³³¹~~GCC~~~~CCC~~ATCG AGAAAACCAT CTCCAAAGCC AAAGGTGGGA CCCGTGGGGT
 1701 GCGAGGGCCA CATGGACAGA GGCCGGCTCG GCCCACCTC TGCCCTGAGA
 1751 GTGACCGCTG TACCAACCTC TGTCCCTACA GGGCAGCCCC GAGAACCACA
 1801 GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG AACCAGGTCA
 1851 GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
 1901 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT
 1951 GCTGGACTCC GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA
 2001 AGAGCAGGTG GCAGCAGGGG AACGTCTTCT CATGCTCCGT GATGCATGAG
 2051 GCTCTGCACA ACCACTACAC GCAGAAGAGC CTCTCCCTGT CTCCGGGTAA
 2101 ATGAGTGC GA CGGCCGGCAA GCCCCCGCTC CCCGGGCTCT CGCGGTGCGA
 2151 CGAGGATGCT TGGCACGTAC CCCCTGTACA TACTTCCCGG GCGCCCAGCA
 2201 TGGAAATAAA GCACCCAGCG CTGCCCTGGG CCCCTGCGAG ACTGTGATGG
 2251 TTCTTTCCAC GGGTCAGGCC GAGTCTGAGG CCTGAGTGGC ATGAGGGAGG
 2301 CAGAGCGGGT CCCACTGTCC CCACACTGGC CCAGGCTGTG CAGGTGTGCC
 2351 TGGGCCCCCT AGGGTGGGGC TCAGCCAGGG GCTGCCCTCG GCAGGGTGGG
 2401 GGATTTGCCA GCGTGGCCCT CCCTCCAGCA GCACCTGCCC TGGGCTGGGC
 2451 CACGGGAAGC CCTAGGAGCC CCTGGGGACA GACACACAGC CCCTGCCTCT
 2501 GTAGGAGACT GTCCTGTTCT GTGAGCGCCC CTGTCCTCCC GACCTCCATG
 2551 CCCACTCGGG GGCATGCCTA GTCCATGTGC GTAGGGACAG GCCCTCCCTC
 2601 ACCCATCTAC CCCCACGGCA CTAACCCCTG GCTGCCCTGC CCAGCCTCGC
 2651 ACCCGCATGG GGACACAACC GACTCCGGGG ACATGCACTC TCGGGCCCTG
 2701 TGGAGGGACT GGTGCAGATG CCCACACACA CACTCAGCCC AGACCCGTTC
 2751 AACAAACCCC GCACTGAGGT TGGCCGGCCA CACGGCCACC ACACACACAC
 2801 GTGCACGCCT CACACACGGA GCCTACCCG GGCGAACTGC ACAGCACCCA

FIGURE 18B (SEQ ID NO. 22)

2851 GACCAGAGCA AGGTCCTCGC ACACGTGAAC ACTCCTCGGA CACAGGCCCC
2901 CACGAGCCCC ACGCGGCACC TCAAGGCCCA CGAGCCTCTC GGCAGCTTCT
2951 CCACATGCTG ACCTGCTCAG ACAAACCCAG CCCTCCTCTC ACAAGGGTGC
3001 CCCTGCAGCC GCCACACACA CACAGGGGAT CACACACCAC GTCACGTCCC
3051 TGGCCCTGGC CCACTTCCCA GTGCCGCCCT TCCCTGCAGG ACGGATCAGC
3101 CTCGACTGTG CCTTCTAGTT GCCAGCCATC TGTTGTTTGC CCCTCCCCCG
3151 TGCCTTCCTT GACCCTGGAA GGTGCCACTC CCACTGTCCT TTCCTAATAA
3201 AATGAGGAAA TTGCATCGCA TTGTCTGAGT AGGTGTCATT CTATTCTGGG
3251 GGGTGGGGTG GGGCAGGACA GCAAGGGGGA GGATTGGGAA GACAATAGCA
3301 GGCATGCTGG GGATGCGGTG GGCTCTATGG CTTCTGAGGC GGAAAGAACC
3351 AGCTGGGGCT CTAGGGGGTA TCCCCACGCG CCCTGTAGCG GCGCATTAAG
3401 CGCGGCGGGT GTGGTGTTA CGCGCAGCGT GACCGCTACA CTTGCCAGCG
3451 CCCTAGCGCC CGCTCCTTTC GCTTTCTTCC CTTCTTTCT CGCCACGTTT
3501 GCCGGGCCTC TCAAAAAAGG GAAAAAAGC ATGCATCTCA ATTAGTCAGC
3551 AACCATAGTC CCGCCCCTAA CTCCGCCCAT CCCGCCCTA ACTCCGCCCA
3601 GTTCCGCCCA TTCTCCGCCC CATGGCTGAC TAATTTTTTT TATTTATGCA
3651 GAGGCCGAGG CCGCCTCGGC CTCTGAGCTA TTCCAGAAGT AGTGAGGAGG
3701 CTTTTTTTGA GGCCTAGGCT TTTGCAAAAA GCTTGGACAG CTCAGGGCTG
3751 CGATTTTCGG CCAAACCTGA CGGCAATCCT AGCGTGAAGG CTGGTAGGAT
3801 TTTATCCCCG CTGCCATCAT GGTTCGACCA TTGAACTGCA TCGTCGCCGT
3851 GTCCCAAAT ATGGGGATTG GCAAGAACGG AGACCTACCC TGGCCTCCGC
3901 TCAGGAACGA GTTCAAGTAC TTCCAAAGAA TGACCACAAC CTCTTCAGTG
3951 GAAGGTAAAC AGAATCTGGT GATTATGGGT AGGAAAACCT GGTTCCTCCAT
4001 TCCTGAGAAG AATCGACCTT TAAAGGACAG AATTAATATA GTTCTCAGTA
4051 GAGAACTCAA AGAACCACCA CGAGGAGCTC ATTTTCTTGC CAAAAGTTTG
4101 GATGATGCCT TAAGACTTAT TGAACAACCG GAATGGCAA GTAAAGTAGA
4151 CATGGTTTGG ATAGTCGGAG GCAGTTCTGT TTACCAGGAA GCCATGAATC
4201 AACCAGGCCA CCTTAGACTC TTTGTGACAA GGATCATGCA GGAATTTGAA
4251 AGTGACACGT TTTTCCAGA AATTGATTG GGGAAATATA AACTTCTCCC
4301 AGAATACCCA GGCGTCCTCT CTGAGGTCCA GGAGGAAAAA GGCATCAAGT

FIGURE 18C (SEQ ID NO. 22)

4351 ATAAGTTTGA AGTCTACGAG AAGAAAGACT AACAGGAAGA TGCTTTCAAG
4401 TTCTCTGCTC CCCTCCTAAA GCTATGCATT TTTATAAGAC CATGGGACTT
4451 TTGCTGGCTT TAGATCTCTT TGTGAAGGAA CCTTACTTCT GTGGTGTGAC
4501 ATAATTGGAC AAACCTACCTA CAGAGATTTA AAGCTCTAAG GTAAATATAA
4551 AATTTTTTAAG TGTATAATGT GTTAAACTAC TGATTCTAAT TGTTTGTGTA
4601 TTTTAGATTTC CAACCTATGG AACTGATGAA TGGGAGCAGT GGTGGAATGC
4651 CTTTAATGAG GAAAACCTGT TTTGCTCAGA AGAAATGCCA TCTAGTGATG
4701 ATGAGGCTAC TGCTGACTCT CAACATTCTA CTCCTCCAAA AAAGAAGAGA
4751 AAGGTAGAAG ACCCCAAGGA CTTTCCTTCA GAATTGCTAA GTTTTTTGAG
4801 TCATGCTGTG TTTAGTAATA GAACTCTTGC TTGCTTTGCT ATTTACACCA
4851 CAAAGGAAAA AGCTGCACTG CTATACAAGA AAATTATGGA AAAATATTCT
4901 GTAACCTTTA TAAGTAGGCA TAACAGTTAT AATCATAACA TACTGTTTTT
4951 TCTTACTCCA CACAGGCATA GAGTGTCTGC TATTAATAAC TATGCTCAAA
5001 AATTGTGTAC CTTTAGCTTT TTAATTTGTA AAGGGGTAA TAAGGAATAT
5051 TTGATGTATA GTGCCTTGAC TAGAGATCAT AATCAGCCAT ACCACATTG
5101 TAGAGGTTTT ACTTGCTTTA AAAAACCTCC CACACCTCCC CCTGAACCTG
5151 AAACATAAAA TGAATGCAAT TGTGTGTGTT AACTTGTTTA TTGCAGCTTA
5201 TAATGGTTAC AAATAAGCA ATAGCATCAC AAATTTTACA AATAAAGCAT
5251 TTTTTTCACT GCATTCTAGT TGTGGTTTGT CCAAATCAT CAATGTATCT
5301 TATCATGTCT GGATCGGCTG GATGATCCTC CAGCGCGGGG ATCTCATGCT
5351 GGAGTTCTTC GCCCACCCCA ACTTGTTTAT TGCAGCTTAT AATGGTTACA
5401 AATAAAGCAA TAGCATCACA AATTTACAA ATAAAGCATT TTTTTCCTG
5451 CATTCTAGTT GTGGTTTGTG CAAACTCATC AATGTATCTT ATCATGTCTG
5501 TATACCGTCG ACCTCTAGCT AGAGCTTGGC GTAATCATGG TCATAGCTGT
5551 TTCCTGTGTG AAATTGTTAT CCGCTCACA TTCCACACAA CATACGAGCC
5601 GGAAGCATAA AGTGTAAGC CTGGGGTGCC TAATGAGTGA GCTAACTCAC
5651 ATTAATTGCG TTGCGCTCAC TGCCCGCTTT CCAGTCGGGA AACCTGTCGT
5701 GCCAGCTGCA TTAATGAATC GGCCAACGCG CGGGGAGAGG CGGTTTGCCT
5751 ATTGGGCGCT CTTCCGCTTC CTCGCTCACT GACTCGCTGC GCTCGGTCGT
5801 TCGGCTGCGG CGAGCGGTAT CAGCTCACTC AAAGGCGGTA ATACGGTTAT

FIGURE 18D (SEQ ID NO. 22)

5851 CCACAGAATC AGGGGATAAC GCAGGAAAGA ACATGTGAGC AAAAGGCCAG
5901 CAAAAGGCCA GGAACCGTAA AAAGGCCGCG TTGCTGGCGT TTTTCCATAG
5951 GCTCCGCCCC CCTGACGAGC ATCACAAAAA TCGACGCTCA AGTCAGAGGT
6001 GGCGAAACCC GACAGGACTA TAAAGATAACC AGGCGTTTCC CCCTGGAAGC
6051 TCCCTCGTGC GCTCTCCTGT TCCGACCCTG CCGCTTACCG GATACCTGTC
6101 CGCCTTTTCTC CCTTCGGGAA GCGTGGCGCT TTCTCAATGC TCACGCTGTA
6151 GGTATCTCAG TTCGGTGTAG GTCGTTGCT CCAAGCTGGG CTGTGTGCAC
6201 GAACCCCCCG TTCAGCCCGA CCGCTGCGCC TTATCCGGTA ACTATCGTCT
6251 TGAGTCCAAC CCGGTAAGAC ACGACTTATC GCCACTGGCA GCAGCCACTG
6301 GTAACAGGAT TAGCAGAGCG AGGTATGTAG GCGGTGCTAC AGAGTTCTTG
6351 AAGTGGTGGC CTAACTACGG CTACACTAGA AGGACAGTAT TTGGTATCTG
6401 CGCTCTGCTG AAGCCAGTTA CCTTCGGAAA AAGAGTTGGT AGCTCTTGAT
6451 CCGGCAAACA AACCACCGCT GGTAGCGGTG GTTTTTTTGT TTGCAAGCAG
6501 CAGATTACGC GCAGAAAAAA AGGATCTCAA GAAGATCCTT TGATCTTTTC
6551 TACGGGGTCT GACGCTCAGT GGAACGAAAA CTCACGTAA GGGATTTTGG
6601 TCATGAGATT ATCAAAAAGG ATCTTCACCT AGATCCTTTT AAATTAAAAA
6651 TGAAGTTTTA AATCAATCTA AAGTATATAT GAGTAAACTT GGTCTGACAG
6701 TTACCAATGC TTAATCAGTG AGGCACCTAT CTCAGCGATC TGTCTATTTT
6751 GTTCATCCAT AGTTGCCTGA CTCCCCGTCG TGTAGATAAC TACGATACGG
6801 GAGGGCTTAC CATCTGGCCC CAGTGCTGCA ATGATACCGC GAGACCCACG
6851 CTCACCGGCT CCAGATTTAT CAGCAATAAA CCAGCCAGCC GGAAGGGCCG
6901 AGCGCAGAAG TGGTCCTGCA ACTTTATCCG CCTCCATCCA GTCTATTAAT
6951 TGTTGCCGGG AAGCTAGAGT AAGTAGTTCG CCAGTTAATA GTTTGCGCAA
7001 CGTTGTTGCC ATTGCTACAG GCATCGTGGT GTCACGCTCG TCGTTTG GTA
7051 TGGCTTCATT CAGCTCCGGT TCCCAACGAT CAAGGCGAGT TACATGATCC
7101 CCCATGTTGT GCAAAAAAGC GGTTAGCTCC TTCGGTCCTC CGATCGTTGT
7151 CAGAAGTAAG TTGGCCGCAG TGTTATCACT CATGGTTATG GCAGCACTGC
7201 ATAATTCTCT TACTGTCATG CCATCCGTAA GATGCTTTTC TGTGACTGGT
7251 GAGTACTCAA CCAAGTCATT CTGAGAATAG TGTATGCGGC GACCGAGTTG
7301 CTCTTGCCCC GCGTCAATAC GGGATAATAC CGCGCCACAT AGCAGAACTT

FIGURE 18E (SEQ ID NO. 22)

7351 TAAAAGTGCT CATCATTGGA AAACGTTCTT CGGGGCGAAA ACTCTCAAGG
7401 ATCTTACCGC TGTGAGATC CAGTTCGATG TAACCCACTC GTGCACCCAA
7451 CTGATCTTCA GCATCTTTTA CTTTCACCAG CGTTTCTGGG TGAGCAAAAA
7501 CAGGAAGGCA AAATGCCGCA AAAAAGGGAA TAAGGGCGAC ACGGAAATGT
7551 TGAATACTCA TACTCTTCCT TTTTCAATAT TATTGAAGCA TTTATCAGGG
7601 TTATTGTCTC ATGAGCGGAT ACATATTTGA ATGTATTTAG AAAAATAAAC
7651 AAATAGGGGT TCCGCGCACA TTTCCCCGAA AAGTGCCACC TGACGTGAC
7701 GGATCGGGAG ATCTGCTAGG TGACCTGAGG CGCGCCGGCT TCGAATAGCC
7751 AGAGTAACCT TTTTTTTTAA TTTTATTTTA TTTTATTTT GAGATGGAGT
7801 TTGGCGCCGA TCTCCCGATC CCCTATGGTC GACTCTCAGT ACAATCTGCT
7851 CTGATGCCGC ATAGTTAAGC CAGTATCTGC TCCCTGCTTG TGTGTTGGAG
7901 GTCGCTGAGT AGTGCGCGAG CAAAATTAA GCTACAACAA GGCAAGGCTT
7951 GACCGACAAT TGCATGAAGA ATCTGCTTAG GGTTAGGCGT TTTGCGCTGC
8001 TTCGCGATGT ACGGGCCAGA TATACGCGTT GACATTGATT ATTGACTAGT
8051 TATTAATAGT AATCAATTAC GGGGTCATTA GTTCATAGCC CATATATGGA
8101 GTTCCGCGTT ACATAACTTA CGGTAAATGG CCCGCCTGGC TGACCGCCCA
8151 ACGACCCCCG CCCATTGACG TCAATAATGA CGTATGTTCC CATAGTAACG
8201 CCAATAGGGA CTTTCCATTG ACGTCAATGG GTGGACTATT TACGGTAAAC
8251 TGCCCCACTG GCAGTACATC AAGTGTATCA TATGCCAAGT ACGCCCCCTA
8301 TTGACGTCAA TGACGGTAAA TGGCCCGCCT GGCATTATGC CCAGTACATG
8351 ACCTTATGGG ACTTTCCTAC TTGGCAGTAC ATCTACGTAT TAGTCATCGC
8401 TATTACCATG GTGATGCGGT TTTGGCAGTA CATCAATGGG CGTGGATAGC
8451 GGTTTGACTC ACGGGGATTT CCAAGTCTCC ACCCCATTGA CGTCAATGGG
8501 AGTTTGTTTT GGCACCAAAA TCAACGGGAC TTTCCAAAAT GTCGTAACAA
8551 CTCCGCCCCA TTGACGCAAA TGGGCGGTAG GCGTGTACGG TGGGAGGTCT
8601 ATATAAGCAG AGCTCTCTGG CTAAGTAGAG AACCCACTGC TTACTGGCTT
8651 ATCGAAATTA ATACGACTCA CTATAGGGAG ACCCAAGCTT

FIGURE 18F (SEQ ID NO. 22)

FIGURE 19 A
(SEQ ID NO. 23)

pd17-hG1b

GGTACCAATTT	TAAATTGATA	TCTCCTTAGG	TCTCGAGTCT	CTAGATPACC	GGTCAATCGA
CCATGGTTAA	ATTTAACTAAT	AGAGGAATCC	AGAGCTCAGA	GATCTATTGG	CCAGTTAGCT
TTGGAATTC	TGCGGCGCGT	TGCTAGACAC	AAGGGCCCAT	CGGTCTTCCC	CTTGGCACCC
AACCTTAAGA	ACGCGGCGGA	ACGATCGTGG	TTCCCGGGTA	GCCAGAAGGG	GGACCGTGGG
TCCTCCAAGA	GCACCTCTGG	GGGCACAGCG	GCCCTGGGCT	GCCCTGTCAA	GGACTTACTTC
AGAGAGTTC	CGTGGAGACC	CCCGTGTGCG	CGGGACCCGA	CGGACCAGTT	CCTGATGAAG
CCCGAACCGG	TGACGGGTGC	GTTGAATCTCA	GGCGCCCTGA	CCAGCGGCGT	GCACACCTTC
GGGCTTGGCC	ACTGCCACAG	CACCTTGAGT	CCGCGGGACT	GGTCGCCGCA	CGTGTGAAG
CCGGCTTGTCC	TACAGTCTTC	AGGACTCTAC	TCCCTCAGCA	GCGTGTAC	CGTGGCCCTCC
GGCCGACAGG	ATGTCAAGAG	TCCTGAGATG	AGGAGTCTGT	CGCACCAATG	GCACGGGAGG
AGCAGCTTGG	GCACCCAGAC	CTACATCTGC	AACGTGAATC	ACAAGCCAG	CAACACCAAG
TCGTCCGAACC	CGTGGGTCTG	GATGTAGACG	TTCACCTTAG	TGTTGGGCTC	GTTGTGCTTC
GTTGGACAAGA	AAGTTGTGA	GAGGCCAGCA	CAGGGAGGGA	GGGTGTCTGC	TGGAAGCCAG
CACCTGTCTCT	TTCACCACT	CTCCGGTCTG	GTCCTTCCCT	CCCACAGACG	ACCTTCGGTC
GCTCAGCCGCT	CCTGCCCTGGA	CGCATCCCGG	CTATGCAGCC	CCAGTCCAGG	GCAGCAAGGC
CGAGTCCGGA	GGACGGACCT	GCGTAGGGCC	GATACGTGGG	GGTCAAGTCC	CGTCTTCCG
AGGCCCCGTC	TGCCCTCTCA	CCCCGAGGCG	TCTGCCCCGC	CCACTTCATGC	TCAGGGAGAG
TCCGGGGCAG	ACGGAGAAGT	GGGCTTCCCG	AGACGGGCGG	GGTGAATACG	AGTCCCTCTC
GGTCTTCTGG	CTTTTTCGCC	AGGCTCTGGG	CAGGCACAGG	CTAGTGGCCC	CTAACCCAGG
CCAGAGAGCC	GAAGAAAGGG	TCCGAGACCC	GTCCGTGTCC	GATCCACGGG	GATTGGGTCC

FIGURE 19B
(SEQ ID NO. 23)

pD17-hG1b

```

610      620      630      640      650      660
CCCTGCACAC AAAGGGGCG GTGCTGGGCT CAGACCTGCC AAGAGCCATA TCCGGGAGGA
GGGACGTGTG TTTCCCGCTC CACGACCCGA GTCTGGACCG TTCTCGGTAT AGCCCTCCT

670      680      690      700      710      720
CCCTGCCCCCT GACCTAAGCC CACCCCAAG GCCAAACTCT CCACCTCCCTC AGCTCGGACA
GGGACGGGGA CTGGATTCCG GTGGGGTTTC CGGTTTGAGA GTGAGGGAG TCGAGCCTGT

730      740      750      760      770      780
CCTTCTCTCC TCCCAGATTTC CAGTAACTCC CAATCTTCTC TTTCGACAGC CCAATCTTTC
GGAAGAGAGG AGGCTCTAAG GTCATTTGAGG GTTAGAAGAG AGACGTCCTG GGTTTAGAAG

790      800      810      820      830      840
TGACAAACTC CACACATGCC CACCGTGCCC AGGTAAGCCA GCCCAGGCTT CGCCCTCCAG
ACTGTTTGA GTGTGTACGG GTGGCACGGG TCCATTCCGT CCGGTCCGGA GCGGAGAGTC

850      860      870      880      890      900
CTCAAGGCGG GACAGGTGCC CTAGAGTAGC CTGCATCCAG GGACAGGCCC CAGCCGGGTG
GAGTCCCGCC CTGTCCACGG GATCTCATCG GACGTAGTTC CCTGTCCGG GTGCGCCAC

910      920      930      940      950      960
CTGACACGTC CACCTCCATC TCTTCTCAG CACCTGAAT CTTGGGGGA CCGTCACTCT
GACTGTGCAG GTGAGGTAG AGAAGAGTTC GTGACTTGA GGCAGTCAGA

970      980      990      1000      1010      1020
TCCCTTTCCT CCCAAAACCC AAGGACACCC TCATGATCTC CCGGACCCCTT GAGGTACAT
AGGAGAAGGG GGGTTTGGG TTCTCTGTCG AGTACTACAG GGCTGGGGA CTTCAGTCTA

1030      1040      1050      1060      1070      1080
GCGTGTGCTG GAGCGTAGC CACGAAGACC CTGAGGTCAA GTTCAACTGG TACGTGACG
CGCACCAACA CCTGCACTCG GTGCTTCTGG GACTCCAGTT CAAGTTGACC ATGCACCTGC

1090      1100      1110      1120      1130      1140
GCGTGGAGGT GCATPATGCC AAGACAAAGC CGCGGAGAGA GCAGTAGAAC AGCAGCTACC
CGCACCTCCA CGTATTACGG TTCTGTTTCG GCGCCCTCCT CGTCATGTTG TCGTGCAATG

1150      1160      1170      1180      1190      1200
GTCTGTCTCAG CGTCCCTACC GTCCCTGCACC AGGACTGGCT GAATGGCAAG GAGTACACAT
CACACCACTC CCAGGAGTGG CAGGACGTGG TCCTGACCCA CTTAACCGTTC CTCTGCTTCA

```

FIGURE 19C
(SEQ ID NO. 23)

PD17-hG1b

327- 1210 1220 1230 327- 1240 1250 1260
GCAAGGCTTC CAACAAGCC CTCACAGCC CCAATCAGAA AACCATCTCC AAAGCCAAAG
CTTCCAGAG GTTGTTCGG GAGGTCGGG GGTACCTCTT TTGATAGAG TTTCCGTTTC
1270 1280 1290 1300 1310 1320
GTGGAGCCCG TGGGTGCGA GGGCCACATG GACAGAGCC GGCTCGGCC ACCCTCTGCC
CACCCTGGGC ACCCCACGCT CCGGTGTAC CTGTCTCCG CCGAGCCGG TGGAGACCG
1330 1340 1350 1360 1370 1380
CTGAGAGTGA CCGCTGTACC AACCTCTGTC CCTACAGGG AGCCCCGAGA ACCACAGTG
GACTCTACAT GGCACATGG TTGAGACAG GGATGTCCCG TCGGGCTCT TGGTGTCCAC
1390 1400 1410 1420 1430 1440
TACACCCCTGC CCCCATCCCG GATGAGCTG ACCAAGAACC AGGTCAGCCT GACCTGCTG
ATGTGGGACG GGGTAGGGC CTAATCGAC TGGTCTTGG TCCAGTCGGA CTGACGGAC
1450 1460 1470 1480 1490 1500
GTCAAGGCT TCTATCCAG CGACATCGCC GTGAGTGGG AGAGCAATGG GCAGCCGGAG
CAGTTCCGA AGATAGGTC GCTGTAGCGG CACCTCACCC TCTCGTTACC CGTCGGCCTC
1510 1520 1530 1540 1550 1560
AACAACTACA AGACCACGCC TCCCGTCTG GACTCCGACG GCTCCTTCTT CCTCTACAG
TTGTTGAIGT TCTGTGCGG AGGCACGAC CTGAGGCTGC CGAGGAAGAA GGAGATGTC
1570 1580 1590 1600 1610 1620
AAGCTACCCG TGGACAAGAG CAGGTGGAG CAGGGGAACG TCTTCTCATG CTCCGTGATG
TTTCAGTGGC ACCGTGTCG GTCCACCGTC GTCCCTTGC AGAAGAGTAC GAGGCACTAC
1630 1640 1650 1660 1670 1680
CATGAGGCTC TGCACAACCA CTACAGCGAG AAGAGCTCT CCTGTCTCC GGGTAAATGA
GTACTCCGAG ACGTGTGCT GATGTGCTC TTCTCGAGA GGGACAGAG CCCATTACT
1690 1700 1710 1720 1730 1740
GTGCGAGCGC CGGCAAGCCC CCGCTCCCG GGCTCTCCG GTCCACAGAG GATGCTTGG
CAGCTGCGC GCCGTGCGG GCGAGGGG CCGAGAGCG CAGCGTCTC CTACGAACCG
1750 1760 1770 1780 1790 1800
ACGTACCCCT TGTACATACT TCCCGGGCGC CCAGCATGA AATAAGCAC CCAGCGCTGC
TGCATGGGG ACATGATGA AGGCGCCGC GGTCTACTT TTAATTCTG GTCTCGGACG

FIGURE 19D
(SEQ ID NO. 23)

PD17-hG1b

```
1810      1820      1830      1840      1850      1860
CCTGGCCCC TGCAGACTG TGATGCTTCT TTCCACGGGT CAGGCCAGT CTGAGGCTG
GGACCCGGGG ACGCTCTGAC ACTACCAAGA AAGGTGCCCA GTCCGGCTCA GACTCCGGAC

1870      1880      1890      1900      1910      1920
AGTGGCAATGA GGGAGGCGA GCGGGTCCCA CTGTCCCCAC ACTGGCCAG GCTGTGCAG
TCACCGTACT CCGTCCGTCT CGCCCAAGGT GACAGGGTG TGACCGGGTC CGACACGTCC

1930      1940      1950      1960      1970      1980
TGATGCTGGG CCCCCCTAGGG TGGGCTTCAG CCAGGGGCTG CCTCGGCAG GGTGGGGAT
ACACGGAACC GGGGGATCCC ACCCCGAGTC GTCCCCCGAC GGGAGCCGTC CCACCCCTTA

1990      2000      2010      2020      2030      2040
TTGCCAGCGT GGGCCCTCCCT CCAGCAGCAC CTGCCCTGGG CTGGGCCACG GGAAGCCCTA
AAGGCTCGCA CCGGGAGGGA GGTCTCTGTG GACGGGACCC GACCCGCTGC CTTTCGGGAT

2050      2060      2070      2080      2090      2100
GGAGCCCTTG GGGACAGACA CACAGCCCTT GCCTCTGTAG GAGACTGTCC TGTCTGTGA
CCTCGGGGAC CCTGTCTGT GTGTGGGGA CGAGACATC CTCTGACAG ACAAGACACT

2110      2120      2130      2140      2150      2160
GGGCCCCCTG CCTCCCCGACC TCCATGCCCA CTCGGGGGCA TGTGTGGGAT GCGGTGGCT
CGCGGGGACA GGAAGGCTGG AGGTACGGGT GAGCCCCCGT ACGACCCCTA CGCCACCCGA

2170      2180      2190      2200      2210      2220
CTATGGCTTC TGAGCGGGA AGAACAGCT GGGGCTCTAG GGGTATCCC CACGGCCCT
GATTAACGAA GCTCCGCCCTT TCTTGTGCGA CCCCAGATC CCCCATAGGG GTGCGGGGA

2230      2240      2250      2260      2270      2280
GTAGCGGGCC ATTTAAGCGG GCGGGTGTGG TGGTTACGCG CAGCGTGACC GCTACACTTG
CATGCCCCCG TAATTTCGCC CGCCACACAC ACCAATGCGC GTGCACTGG CGATGTGAAC

2290      2300      2310      2320      2330      2340
CCAGCGCCCT AGCGCCCGCT CCTTTCGCTT TCTTCCCTTC CTTTCTGCGC ACGTTCGCG
GCTCGCGGGA TCGCGGGCGA GGAAGCGAA AGAAGGGAAG GAAAGACCG TGCAAGCGGC

2350      2360      2370      2380      2390      2400
GCTTTCCTCG TCAAGCTCTA AATCGGGGCA TCCCTTTAGG GTTCCGATT T AGTGCTTTAC
CGAAGGGGCG AGTTCGAGAT TTAGCCCGCT AGGGAATCC CAAGCTAAA TCACGAATG
```

FIGURE 19E
(SEQ ID NO. 23)

PD17-hG1b

2410	2420	2430	2440	2450	2460
GGCACCCTCGA	CCCCAAAAA	CTTGATTAGG	GTGATGGTTC	ACGTAGTGG	CCATGCCCT
CCGTGAGCT	GGGGTTTTT	GAACTAATCC	CACTAACCAAG	TGCATCACC	GGTAGCGGA
2470	2480	2490	2500	2510	2520
GATGACCGT	TTTTGCCCT	TTGACGTTGG	AGTCCACGTT	CTTTAATAGT	GGACTCTTGT
CTATCTGCCA	AAAAGCGGA	AACTGCACAC	TCAGGTGCA	GAAATTATCA	CCTGAGACA
2530	2540	2550	2560	2570	2580
TCCAAACCTGG	AACAACACTC	AACCCCTATCT	CGGTCTATTTC	TTTTTGATTTA	TAAGGATTT
AGGTTTGACC	TTGTTGTGAG	TTGGGATPAGA	GCCAGATPAG	AAAACTPAAT	ATTCCCTPAA
2590	2600	2610	2620	2630	2640
TGGGGAATTC	GGCCPATTGG	TTTAAAAATG	AGCTGATTTA	ACAAAAATTT	AACGCGAATT
ACCCCTPAAAG	CCGGATPACC	AATTTTGTAC	TCGACTPAAT	TGTTTTTAAA	TTGCGCTTAA
2650	2660	2670	2680	2690	2700
AATTCGTGG	AATGCTGTC	AGTTAGGGTG	TGGAAGTCC	CCAGGCTCCC	CAGGCAAGCA
TTAAGACACC	TTACACACAG	TCAATCCCAC	ACCTTTCAGG	GGTCCGAGGG	GTCCGTCCGT
2710	2720	2730	2740	2750	2760
GAAGTATGCA	AAGCATGCAT	CTCAATTAGT	CAGCAACCAT	AGTCCCGCCC	CTAATCCGC
CTTCATPACGT	TTCTPACGTA	GAGTTAATCA	GTCTGTGTA	TCAGGGCGGG	GATTGAGCG
2770	2780	2790	2800	2810	2820
CCATCCCCGCC	CCTPACTCCG	CCCAGTTCGG	CCCATTCTCC	GCCCCATGGC	TGACTPAAATT
GGTAGGGCGG	GGATTGAGGC	GGGTCAAGGC	GGGTAAGAGG	CGGGTACC	ACTGATYAAA
2830	2840	2850	2860	2870	2880
TTTTTATTTA	TGCAGAGGCC	GAGGCCGCCCT	CGGCTCTGA	GCTATTCCAG	AAGTAGTAG
AAAAATPAAAT	ACGTCTCCGG	CTCCGGCGGA	GCCGGAAGCT	CGATPAGGTC	TTTCATCACTC
2890	2900	2910	2920	2930	2940
GAGGCTTTTTT	TGGAGGGCTTA	GGCTTTTGA	AAAAGCTTGG	ACAGCTCAGG	GCTGCGAATT
CTCCGAAAAA	ACCTCCGGAT	CCGAAAAAGT	TTTTTCGAAC	TGTCGAGTCC	CGACGCTPAA
2950	2960	2970	2980	2990	3000
CGGCGCAAC	TTGACCGCAA	TCCPAGCGTG	AAGGCTGTA	GGATTTTATC	CCGCGTCCA
GCGCGTTTG	AACTGCCGTT	AGGATCGCAC	TTCCGACCAT	CCTAAAAATAG	GGGCGACGTT

FIGURE 19F
(SEQ ID NO. 23)

pD17-hG1b

TCATGCTTCG	3010	ACCATTGAAC	3020	TGCATCGTCG	3030	CCGTGTCCCA	3040	AAATATGGGG	3050	ATTGCCAAGA	3060
AGTACCACAGC		TGCTAACTTG		ACGTAGCAGC		GGCACAGGGT		TTTATACCCC		TAAACGTTCT	
ACGGAGACCT	3070	ACCCTGGCCT	3080	CCGCTCAGGA	3090	ACGAGTTCAA	3100	GTACTTCCAA	3110	AGAAATGACCA	3120
TGCTCTTGGA		TGGGACCCGA		GGCGAGTCCT		TGCTCAAGTT		CATGAAGTTT		TCTTACTGGT	
CAACCTCTTC	3130	AGTGGAGAGT	3140	AAACAGATC	3150	TGGTGATTTAT	3160	GGGTAGGAAA	3170	ACCTGGTTCT	3180
GTTGGAGAAG		TCACCTTCCA		TTTGTCTTAG		ACCACTAATA		CCCATCCCTT		TGGACCAAGA	
CCATTTCCTGA	3190	GAAGAAATCGA	3200	CCTTTAAAGG	3210	ACAGAATTAA	3220	TATAGTTCTC	3230	AGTAGAGAAC	3240
GTTAAGGACT		CTTCTTAGCT		GGAATTTTCC		TGCTTTAATT		ATATCAAGAG		TCATCTCTTG	
TCAAAGAACCC	3250	ACCACGAGGA	3260	GCTCATTTTTC	3270	TGCGCAAAAG	3280	TTTGGATGAT	3290	GCCTTAAGAC	3300
AGTTTCTTGG		TGGTGCTCCT		CGAGTAAAG		AACGGTTTTC		AAACCTACTA		CGGAATTC TG	
TTTATTGAACA	3310	ACCGGAATTG	3320	GCAAGTAAAG	3330	TAGACATGGT	3340	TTGGATAGTC	3350	GGAGGCAGTT	3360
AATACTTGT		TGGCCTTAAC		CGTTCATTTT		ATCTGTACCA		AACCTATCAG		CCTCCGTCAA	
CTGTTTACCA	3370	GGAAGCCATG	3380	AATCAACCAG	3390	GCCACCCTTAG	3400	ACTCTTTGTC	3410	ACAAGGATCA	3420
GACAAANGGT		CCTTCGGTAC		TTAGTGTGTC		CGGTGGAATC		TGAGAAACAC		TGTTCTTAGT	
TGCAGGAATT	3430	TGAAAGTGAC	3440	ACGTTTTC	3450	CAGAAATTGA	3460	TTTTGGGAAA	3470	TATTAACCTTC	3480
ACGTCCCTAA		ACTTTCAC TG		TGCCAAAAAG		GTCTTAACT		AAACCCCTTT		ATATTGAAG	
TCCCAGAAATA	3490	CCCAGGCGTC	3500	CTCTCTGAGG	3510	TCCAGAGAGA	3520	AAAAGGCATC	3530	AAGTATTAACT	3540
AGGCTCTTAT		GGGTCCGCGAG		GAGAGACTCC		AGGTCTCTCT		TTTTCCGTAG		TTCAATATCA	
TTGAGTCTTA	3550	CGAGAAGAAA	3560	GACTTAACAGG	3570	AAGATGCTTT	3580	CAAGTTCTCT	3590	GCTCCCTCTC	3600
AACCTCAGAT		GCTCTCTCTTT		CTGATGTCTC		TTCTACGAAA		GTTCAAGAGA		CGAGGGGAGG	

FIGURE 19C
(SEQ ID NO. 23)

pD17-hG1b

3610	3620	3630	3640	3650	3660
TTAAGCTAATG	CATTTTATTA	AGACCATGG	ACTTTTGCTG	GCTTTAGATC	TCTTTGTGAA
ATTTCGATAC	GTAATAATAT	TCTGGTACCC	TGAATAACGAC	CGAATCTAG	AGAAACACTT
3670	3680	3690	3700	3710	3720
GGAACCTTAC	TTCTGTGGTG	TGACATAATT	GGACAAACTA	CCTTACAGAGA	TTTAAAGCTC
CCTTGGAAATG	AAGACACCCAC	ACTGTATTAA	CCTGTTTGAT	GGATGTCCT	AAATTTTCGAG
3730	3740	3750	3760	3770	3780
TAAAGTAAAT	ATAAATTTT	TAAGTGTATA	ATGTGTAA	CTACTGATTC	TAATTTGTTTG
ATTCCATTTA	TATTTTAAAA	ATTACATAT	TACACAATTT	GATGACTAAG	ATTAAACAAC
3790	3800	3810	3820	3830	3840
TGTATTTTAG	ATTCCAACCT	ATGGAACCTGA	TGAATGGGAG	CAGTGTGGA	ATGCCCTTTAA
ACATPAAAAATC	TAAAGTTGGA	TACCTTGACT	ACTTACCCTC	GTCACCACT	TACGGAATTT
3850	3860	3870	3880	3890	3900
TGAGGAAAAAC	CTGTTTGTCT	CAGAAGAAAT	GCCATCTAGT	GATGATGAGG	CTACTGCTGA
ACTCCTTTTG	GACAAAAACGA	GTCCTTCTTA	CGGTAGATCA	CTACTACTCC	GATGACGACT
3910	3920	3930	3940	3950	3960
CTCTCAACAT	TCTACTCCTC	CAAAAAAGAA	GAGAAAGTA	GAAGACCCCA	AGGACTTTCC
GAGAGTTGTA	AGATGAGGAG	GTTTCTTCT	CTCTTCCAT	CTTCTGGGGT	TCCTGAAGG
3970	3980	3990	4000	4010	4020
TTTCAGAAATG	CTAAGTTT	TGAGTCATGC	TGTTTAT	AATAGAATC	TTGCTTGCTT
AAGTCTTAAC	GATTCAAAA	ACTCAGTACG	ACACAAATCA	TTATCTTGAG	AACGAACGAA
4030	4040	4050	4060	4070	4080
TGCTATTTTAC	ACCACAAGG	AAAAAGCTGC	ACTGCTATAC	AAGAAAAATTA	TGGAATAATA
ACGATPAAATG	TGGTGTTC	TTTTTCGACG	TGACGATATG	TTCTTTTAAT	ACCTTTTAT
4090	4100	4110	4120	4130	4140
TTTCTGTAAC	TTTATTAAGTA	GGCATTAACAG	TTTATTAATCAT	AACATACTGT	TTTTTCTTAC
AAGACATTCG	AAATATTCAT	CCGTATTGTC	AATATTAAGTA	TTGTATGACA	AAAAAGAATG
4150	4160	4170	4180	4190	4200
TCCACACAGG	CATAGAGTGT	CTGCTATTAA	TAACTATGCT	CAAAAATTGT	GTACCTTTAG
AGGTGTTC	GTATCTCACA	GACGATTAAT	ATTGATACGA	GTTTTTAACA	CATGNAATC

FIGURE 19H
(SEQ ID NO. 23)

PD17-hG1b

4210	4220	4230	4240	4250	4260
CTTTTAAATT	TGTAAGGGG	TTAATAAGSA	ATATTGATG	TATAGTCCCT	TGACTAGAGA
GAAAAATTAA	ACATTTCCT	AATTATTCCT	TATTAACCTAC	ATATCACGGA	ACTGATCTCT
4270	4280	4290	4300	4310	4320
TCATTAATCAG	CCATACCACA	TTTGTAAGAG	TTTTACTTGC	TTTAAAAAAC	CTCCACACAC
AGTATTAGTC	GGTATGGTGT	AAACATCTCC	AAAATGAACG	AAATTTTGTG	GAGGATGTGG
4330	4340	4350	4360	4370	4380
TCCCCCTGAA	CCTGAACAT	AAAATGAATG	CAATTGTTGT	TGTTAACTTG	TTTATTTGCAG
AGGGGACTT	GGACTTGTGTA	TTTACTTAC	GTTAACACACA	ACAATTGAAC	AAATTAACGTC
4390	4400	4410	4420	4430	4440
CTTATAATGG	TTTACAATAA	AGCAATAGCA	TCACAAATTT	CACAAATAAA	GCATTTTTTTT
GAATATTACC	AATGTTTATT	TGCTTATCGT	AGTGTTTAAA	GTTGTTTATT	CGTAAAAAAA
4450	4460	4470	4480	4490	4500
CACTGCATTC	TAGTTGTGT	TTGTCCAAAC	TCATCAATGT	ATCTTATCAT	GTCGTGATCG
GTGACGTAAG	ATCAACACCA	AACAGTTTG	AGTAGTTACA	TAGAATAGTA	CAGACCTAGC
4510	4520	4530	4540	4550	4560
GCTGGATGAT	CCTCCAGCCG	GGGATCTCA	TGCTGAGTT	CTTCGCCAC	CCCACTTGT
CGACCTACTA	GGAGTCCGC	CCCCTAGAGT	ACGACCTCAA	GAAAGGGTG	GGGTTGAACA
4570	4580	4590	4600	4610	4620
TTATTCACAGC	TTTATTAATGT	TACAATAAAA	GCAATAGCAT	CACAAATTTT	ACAAATTAAG
AATTAACGTCG	AATATTACCA	ATGTTTATTT	CGTTATCGTA	GTTGTTAAAG	TGTTTATTTT
4630	4640	4650	4660	4670	4680
CAATTTTTC	ACTGCATTC	AGTTGTGTT	TGTTCCAACT	CATCAATGTA	TCTTATTCATG
GTAATAAAG	TGACGTAAGA	TCAACACCAA	ACAGGTTTGA	GTAATTACAT	AGAATAGTAC
4690	4700	4710	4720	4730	4740
TCTGTATACC	GTCGACCTCT	AGCTAGAGCT	TGGCGTAATC	ATGTCATAG	CTGTTTCTTG
AGACATATGG	CAGCTGAGA	TGCACTCTCGA	ACCGCATTAG	TACCAGTATC	GACAAAGGAC
4750	4760	4770	4780	4790	4800
TGTGAATTTG	TTATCCGCTC	ACAAATTCAC	ACAACATAGC	AGCCGGAAGC	ATTAAGTGT
ACACTTTAAC	AATAGGCGAG	TGTTAAGGTG	TGTTGTATGC	TGCGCCTTGC	TATTTCACAT

FIGURE 191
(SEQ ID NO. 23)

PD17-hG1b

```
4810      4820      4830      4840      4850      4860
AAGCCYGGG  TGCCTAATGA  GTGAGCTAAC  TCACATTAAT  TGCCTTGGC  TCACCTGCCG
TTCGACCC   ACGATTAAT  CACTCGATTG  AGTGTAAATTA  ACGCAACGC  AGTACGGGC

4870      4880      4890      4900      4910      4920
CTTCCAGTC  GGAACCTG  TCGTGCCAGC  TGCATTAAATG  AATCGCCAA  CGCGCGGGA
GAAAGGTCAG  CCTTTGAC  AGCAGGTCG  ACGTAATTAC  TTAGCCGTT  GCGGCCCTT

4930      4940      4950      4960      4970      4980
GAGCGGTTT  GCGTATTGG  CGCTCTTCCG  CTTCCTCGCT  CACTGACTCG  CTGCGTCGG
CTCCGCCAA  CGCATTAACC  GCGAGAAGGC  GAAGAGCGA  GTGACTGAG  GACCGAGCC

4990      5000      5010      5020      5030      5040
TCGTTGCGCT  GCGGCGAGCG  GTATTCAGCTC  ACTCAAGGC  GGTAAATACGG  TTATTCACAG
AGCAAGCCGA  CGCCGCTCG  CATAGTCGAG  TGAATTTCG  CCATTATGCC  AATAGGTCG

5050      5060      5070      5080      5090      5100
AATCAGGGGA  TAACCGCAGA  AAGAACAATGT  GAGCAAAAG  CCAGCAAAAG  GCCAGAAC
TTAGTCCCT  ATGCGTCTT  TTCTGTATACA  CTCGTTTCC  GGTGTTTTT  CGGTCTTGG

5110      5120      5130      5140      5150      5160
GTAAAAAGC  CGCGTTGCTG  GCGTTTTC  ATAGGCTCCG  CCCCCCTGAC  GAGCATACACA
CATTTTCCG  GCGCAACGAC  CGCAAAAAGG  TATCCGAGGC  GGGGGACTG  CTCGTAGTGT

5170      5180      5190      5200      5210      5220
AAAATCGACG  CTCAGTCAG  AGGTGGCGAA  ACCCGACAGG  ACTATTAAGA  TACCAGGCT
TTTTAGCTGC  GAGTTCAGTC  TCCACCGCTT  TGGGCTGTCC  TGATATTTC  ATGTCCGCA

5230      5240      5250      5260      5270      5280
TTCCCCCTG  AAGCTTCCTC  GTGCGCTTC  CTGTTCGAC  CCTGCCGCTT  ACCGATACC
AAGGGGACC  TTCGAGGAG  CACCGAGAG  GACAAGGCTG  GGACGGCGAA  TGGCCTATGG

5290      5300      5310      5320      5330      5340
TGTCCGCTT  TCTCCCTTCG  GGAAGCGTGG  CGCTTCTCA  ATGCTACGC  TGTAGGTATC
ACAGGCGGAA  AGAGGGAAG  CCTTCGACCC  GCGAAAGAGT  TACGAGTGG  ACATCAATAG

5350      5360      5370      5380      5390      5400
TCAGTTCCGT  GTAGGTCTT  CGCTCCAAAG  TGGGCTGTGT  GCACGAACCC  CCCGTTACG
AGTCAAGCCA  CATCCAGCAA  GCGAGTTGG  ACCCGACACA  CGTGCTTGG  GGGCAAGTCG
```

FIGURE 19J
(SEQ ID NO. 23)

pD17-hG1b

5410	5420	5430	5440	5450	5460
CCGACCGCTG	CGCCTTATCC	GGTAACATATC	GTCTTGAGTC	CAACCCGGTA	AGACACGACT
GGCTGGCGAC	GGGAAATAGG	CCATTGATAG	CAGAACTCAG	GTGGGCCAT	TCTGTGCTGA
5470	5480	5490	5500	5510	5520
TATCGCCCACT	GGCAGCAGCC	ACTGCTAACA	GGATTAGCAG	AGCAGGTAAT	GTAGGCGGTG
ATAGCGGTGA	CCGTGCTCGG	TGACCATTTGT	CCTAATCGTC	TGCTTCATA	CATCCGCCAC
5530	5540	5550	5560	5570	5580
CTTACAGAGTT	CTTGAAGTGG	TGGCCTTAAT	ACGGCTACAC	TAGAAGGACA	GTAATTGGTA
GATGTCACAA	GAACCTCAC	ACCGGATTGA	TGCCGATGTG	ATCTTCCTGT	CAATAAACCAT
5590	5600	5610	5620	5630	5640
TCTGCGCTCT	GCTGAAGCCA	GTTACCTTTCG	GAAAAAGAGT	TGGTAGCTCT	TGATCCGCA
AGACGGCAGA	CGACTTCGGT	CAATGGAAGC	CTTTTCTCTCA	ACCATCGAGA	ACTAGGCCGT
5650	5660	5670	5680	5690	5700
AACAACCCAC	CGCTGGTAGC	GGTGGTTTTT	TTGTCTGCAA	GCAGCAGATT	ACCGCGAGAA
TTGTTTGTG	GGACCAATCG	CCACCAAAAA	AACAACGTT	CGTGTCTTAA	TGCGCGTCTT
5710	5720	5730	5740	5750	5760
AAAAAGGATC	TCAAGAAGAT	CCTTTGATCT	TTTCTACGGG	GTCTGACGCT	CAGTGAACG
TTTTTTCCTAG	AGTTCCTTCA	GGAACTAGA	AAAGATGCC	CAGACTGCGA	GTACACTTGC
5770	5780	5790	5800	5810	5820
AAACCTCACG	TTAAGGATTT	TTGGTCATGA	GATTATCAAA	AAGGATCTTC	ACCTTAGATCC
TTTTTGAGTCC	AATTCCCTAA	AACCACTACT	CTAATAGTTT	TTCTTAGAAG	TGGATCTAGG
5830	5840	5850	5860	5870	5880
TTTTTAATTTA	AAAATGAAGT	TTTTAAATCAA	TCTAAAGTAT	ATATGAGTAA	ACTTGTCTTG
AAAAATTTAAT	TTTTTACTTCA	AAATTTAGTT	AGATTTCATA	TATACTCATTT	TGAACACAGAC
5890	5900	5910	5920	5930	5940
ACAGTTACCA	ATGCTTAATC	AGTGAAGCAC	CTATCTCAGC	GATCTGTCTA	TTTTGTTTCAAT
TGTCATATGCT	TACGAATTAG	TCACTCCGTG	GATAGAGTGG	CTAGACAGAT	AAAGCAAGTGA
5950	5960	5970	5980	5990	6000
CCATAGTTGC	CTGACTCCCC	GTGCTGTAGA	TAACTPACGAT	ACGGGAGGGC	TTACCATCTG
CGTATCAACG	GACTGAGGGG	CAGCACATCT	ATTGATGCTA	TGCCCTCCCG	AATGGTAGAC

FIGURE 19K
(SEQ ID NO. 23)

pD17-hG1b

```
6010      6020      6030      6040      6050      6060
GCCCCAGTGC TGCATGATA CCGGAGACC CACGCTCACC GGCTCCAGAT TTATCAGCAA
CGGGGTACG ACGTACTAT GCGCTCTGG GTGCGAGTGG CCGAGTCTA AATAGTCGT

6070      6080      6090      6100      6110      6120
TAAACCAAGC AGCCGGAAG GCGGAGCGA GAAGTGTCC TCGAAGTTTA TCCGCTCCA
ATTGGTCGG TCGCCTTCC CGGCTCGCGT CTTACACAGG ACGTTGAAT AGCGGAGGT

6130      6140      6150      6160      6170      6180
TCCAGTCTAT TAATGTGTC CGGGAAGCTA GAGTAACTAG TTCGCCAGTT AATAGTTGC
AGGTCAGATA ATTAACAAC GCGCTTCGAT CTCATTCAAT AAGCGTCAA TTATCAAACG

6190      6200      6210      6220      6230      6240
GCAACGTTGT TGCCATTGCT ACAGGCATCG TGGTGTACG CTCGTGCTT GGTATGCTT
CGTTGCAACA ACGGTAAAG TGTCCGTAGC ACCACAGTGC GAGCAGCAAA CCATACCGAA

6250      6260      6270      6280      6290      6300
CATTCAGCTC CGGTTCCCAA CGATCAAGGC GAGTTACATG ATCCCCCATG TTGTGCAAAA
GTAAGTCGAG GCCAAGGTT GCTAGTCCG CTCATGTAC TAGGGGGTAC AACACGTTTT

6310      6320      6330      6340      6350      6360
AAGCGGTTAG CTCCTTCGGT CCTCCGATCG TTGTCAAGAG TAAGTTGGCC GCAGTGTAT
TTCGCCAATC GAGGAAGCCA GGAGGCTAGC AACAGTCTTC ATTCAACCGG CGTCACAATA

6370      6380      6390      6400      6410      6420
CACTCAATGT TATGGCAGCA CTGCATTAAT CTCTTACTGT CATGCCATCC GTAAGATGCT
GTGAGTAACA ATACCGTCGT GACGTATTAA GAGAAATGACA GTACGGTAGG CATTCACGA

6430      6440      6450      6460      6470      6480
TTTCTGTGAC TGGTAGTAC TCAACCAAGT CATTCGTAGA ATAGTGTATG CGGCAGCCGA
AAAGACACTG ACCACTCATG AGTTGGTTCA GTAAGACTCT TATCACAATAC GCCGCTGGCT

6490      6500      6510      6520      6530      6540
GTTGCTCTTG CCGGCGCTCA ATACGGGATA ATACCGCGCC ACAATAGCAGA ACTTTAAAG
CAACGAGAAC GGGCCGCAAT TATGCCCTAT TATGGCGCGG TGTATCGTCT TGAATTTTC

6550      6560      6570      6580      6590      6600
TGCTCATCAT TGGAAACGT TCTTCGGGGC GAAAAGTCTC AAGGATCTTA CCGCTGTGA
ACGAGTAATA ACCTTTGCA AGAAGCCCCG CTTTGTAGAG TTCTAGAAAT GGCACAACT
```

FIGURE 19L
(SEQ ID NO. 23)

pD17-hG1b

6610	6620	6630	6640	6650	6660
GATCCAGTTC	GATGTAAACC	ACTCGTCAC	CCAACGTATC	TTACAGCATCT	TTTACTTTCA
CTAGGTCAAG	CTACATTTGG	TGAGCACGTG	GGTTGACTAG	AAGTCGTAGA	AAATGAAGT
6670	6680	6690	6700	6710	6720
CCAGCGTTTC	TGGGTGAGCA	AAAACAGGAA	GGCAAAATGC	CGCAAAAAG	GGAATTAAGG
GGTCGCAAAG	ACCCACTCGT	TTTGTCCCTT	CCGTTTACG	GCGTTTTC	CCTTATTTCC
6730	6740	6750	6760	6770	6780
CGACACGGAA	ATGTTGAATTA	CTCATCTCTT	TCCTTTTCA	ATATTATTGA	AGCATTTATC
GCTGTGCCCTT	TACAACTTAT	GAGTATGAGA	AGGAAAAGT	TATTAATTAAT	TGCTAAATAG
6790	6800	6810	6820	6830	6840
AGGCTTATTG	TCTCATGAGC	GGATACATAT	TTGATGTAT	TTAGAAAAT	AAACAATAG
TCCCAATTAAC	AGAGTACTCG	CCTATGTATA	AACTTACATA	AATCTTTTTA	TTTGTTTATC
6850	6860	6870	6880	6890	6900
GGTTCGCCG	CACATTTCCT	CGAAAAGTGC	CACCTGACGT	CGACGGATCG	GGAGATCTGC
CCCAAGGCGC	GTGTAAGGG	GCTTTTCACG	GTGACTGCA	GCTGCCTAGC	CCTCTAGACG
6910	6920	6930	6940	6950	6960
TAGGTGACCT	GAGCGCGCC	GGCTTCGAAT	AGCCAGAGTA	ACCTTTTATT	TTTAATTTTAT
ATCCACTGGA	CTCCGCGCG	CCGAAGCTTA	TGCGTCTCAT	TGGAAAAAA	AAATTAATAA
6970	6980	6990	7000	7010	7020
TTTTATTATT	TTTTGAGATG	GAGTTTGGCG	CCGATCTCCC	GATCCCCAT	GGTCGACTCT
AAATTAATAA	AAAACCTTAC	CTCAAAACCG	GGCTAGAGGG	CTAGGGGATA	CCAGCTGAGA
7030	7040	7050	7060	7070	7080
CAGTACAATC	TGCTCTGATG	CCGCAATGTT	AAAGCAGTAT	CTGCTCCCTG	CTTGTGTGTT
GTCAATGTAG	ACGAGACTAC	GGCGTATCAA	TTCCGTGATA	GACGAGGGAC	GAACACACAA
7090	7100	7110	7120	7130	7140
GGAGTTCGCT	GAGTAGTGGC	CGAGCAAAAT	TTAAGCTACA	ACAAGGCAAG	GCTTGACCGA
CCTCCAGCGA	CTCATCACGC	GCTCGTTTTA	AATTCGATGT	TGTTCCGTTT	CGAAGTGGCT
7150	7160	7170	7180	7190	7200
CAATTGCATG	AAGAATCTGC	TTAGGGTTAG	GCGTTTTCG	CTGCTTCGCG	ATGTACGGGC
GTTAACGTAC	TTCCTTAGACG	ATCCCAATC	CGCAAAACGC	GACGAAAGCG	TACATGCCCC

FIGURE 19M
(SEQ ID NO. 23)

pD17-hG1b

7210	7220	7230	7240	7250	7260
CAGATATACG	CGTTGACATT	GATTATTGAC	TAGTTATTAA	TAGTAATCAA	TTACGGGCTC
GTCCTATATGC	GCAACTGTAA	CTAATAACTG	ATCATAAATT	A1CATTTAGTT	AATGCCCCAG
7270	7280	7290	7300	7310	7320
ATTAGTTTCA	AGCCCATATA	TGGAGTTCCG	CGTTACATAA	CTTACGGTAA	ATGCCCCGCC
TAATCAAGTA	TGCGGTATAT	ACCTCAAGGC	GCAATGTATT	GAATGCCATT	TACCGGGCGG
7330	7340	7350	7360	7370	7380
TGGCTGACCG	CCCAACGACC	CCCCGCCATT	GACGTCAATA	ATGACGTAAG	TTCCCATAGT
ACCGACTVGG	GGGTGCTGG	GGGCGGGTAA	CTGCAGTTAT	TACTGCATTAC	AAAGGTATCA
7390	7400	7410	7420	7430	7440
AACGCCAATA	GGGACTTTC	ATTGACGTCA	ATGGGTGAC	TATTTACGGT	AAACTGCCCA
TTGCGGTTAT	CCCTGAAGG	TAACTGCAGT	TACCCACCTG	ATAAATGCCA	TTTGACGGGT
7450	7460	7470	7480	7490	7500
CTTGGCAGTA	CATCAAGTGT	ATCATATGCC	AAGTACGGCC	CCTATTGACG	TCAATGACGG
GAACCGTCAT	GTAATTGACA	TAGTATACGG	TTTCATGCGGG	GGATAACTGC	AGTTACTGCC
7510	7520	7530	7540	7550	7560
TAAATGGCCC	GCCTGGCATT	ATGCCCAGTA	CATGACCTTA	TGGGACTTTC	CTACTTGGCA
ATTTACCGGG	CGGACCGTAA	TACGGGTCA	GTACTGGAAT	ACCTGAAG	GATGAACCGT
7570	7580	7590	7600	7610	7620
GTACATCTAC	GTATTAGTCA	TCCCTATTAC	CATGTGATG	CGGTTTGGC	AGTACATCAA
CATGTAGATG	CATAATCAGT	AGCGATAATG	GTACCACTAC	GCCAAAACCG	TCACTGTAATT
7630	7640	7650	7660	7670	7680
TGGGCGTGA	TAGCGTTTG	ACTCAGGGGG	ATTTCGAAGT	CTCCACCCCA	TTGACGTCAA
ACCCGCACCT	ATCGCCAAAC	TGAGTGCCCC	TAAAGGTTCA	GAGGTGGGGT	AACTGCAGTT
7690	7700	7710	7720	7730	7740
TGGGAGTTTG	TTTTGGCACC	AAAAATCAACG	GGACTTTCOA	AAATGTGTA	ACAACTCCGC
ACCCYCAANC	AAAACCGTGG	TTTTAGTTGC	CCTGAAGGT	TTTACAGCAT	TGTTGAGCGG
7750	7760	7770	7780	7790	7800
CCCATGTGACG	CAATATGGCG	GTAAGCGTGT	ACGGTGGAG	GTCTATATTA	GCAGAGCTCT
GGGTAACATGC	CTTTACCCGC	CATCCGCACA	TGCCACCCCTC	CAGATATATTT	CGTCTCGAGA

FIGURE 19N
(SEQ ID NO. 23)

PD17-hG1b

7810	7820	7830	7840	7850	7860
CTGGCTPACT	AGAGAACCCA	CTGCTTACTG	GCTTATCGAA	ATTATATACGA	CTCACTATATAG
GACCGATTGA	TCTCTTGGGT	GACGAATGAC	CGAATAGCTT	TAATTATGCT	GAGTGATATC
7870	7880				
GGAGACCCCAA	GCTT				
CCTCTGGGTT	CGAA				

Figure 26

hBR96-2 Heavy Chain Variable Region (VH)

1 11 21 31 41
 EVQLVESGGG LVQPGGSLRL SCAASGPFPS DYMYWVRQA PGKGLEWVSY
 51 61 71 81 91
 ISQDGDITDY ADSVKGRFTI SRDNAKNSLY LQMNSLRDED TAVYYCARGL
 101 111
 ADGAWFAYWG QGTLVTVSS (SEQ ID NO. 24)

human IgG1 constant

CH1
 A STKGPSVFPL APSSKSTSGG TAALGCLVKD
 YFPEPVTVSW NSGALTSGVH TFPVQLQSSG LYSLSSTVTV PSSSLGTQTY
 ICNVNKKPSN TKVDKKVEPK SCDKTHCTCP CH2 133 233
 DTLNISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS
 TYRVSSTLTV LKQDNLNGKE YKDKVSNKAL PAKLEKTISK AKGQPREPQV
 YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTTPVL
 DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK
 (SEQ ID NO. 25)

Figure 27

hBR96-2A: Heavy Chain Variable Region (VH)

1 11 21 31 41
EVQLVESGGG LVQPGGSLRL SCAASGFPFS DYYMYWVRQA PGKGLEWVS
51 61 71 81 91
ISQDGDITDY ADSVKGRFTI SRDNAKNSLY LQMNSLRDED TAVYYCARGL
101 111
ADGAWFAYWG QGTLVTVSS (SEQ ID NO. 24)

hBR96-2A: Human Heavy Chain IgG1 Constant Region Δ CH2

A STKGPSVFPL APSSKSTSCG TAALGCLVKD YFPEPVTVSW NSGALTSGVH
TFPAVLQSSG LYSLSVVTV PSSSLGTQTY ICNVNHKPSN TKVDKKVEPK
SCDKTHTCPP CP GQPREPQV YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA
VEWESNGQPE NNYKTTTPVL DSDGSFFLYS KLTVDKSRWQ QGNVFSCSV
HEALHNHYTQ KSLSLSPGK (SEQ ID NO. 26)

Figure 28

This sequence is the chi BR96 IgG1 with CH2 deleted.

VH
1 EVNLVESGGG LVQPGGSLKV SCVTSGFTFS DYYMYWVRQT PEKRLEWVAY
51 ISQGGDITDY PDTVKGRFTI SRDNAKNTLY LQMSRLKSED TAMYICARGL
101 DDGAWFAYWG QGTLVTVSWA STRGPSVFPL APSSKSTSGG TAALGCLVKD
151 YFPEPVTVSW NSGALTSGVH TFP AVLQSSG LYSLSVVTV PSSSLGTQTY
201 ICNVNHHKPSN TKVDKKVEPK SCDKTHTCPP CH³QPREPQV YTLPPSRDEL
251 TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPFVL DSDGSFFLYS
301 KLTVDKSRWQ QGNVFSCSVN HEALHNHYTQ KSLSLSPGK

(SEQ ID NO. 27)